

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 22, 2004, 18:05:37 ; Search time 55 Seconds  
(without alignments)  
1848.051 Million cells updates/sec

Title: US-09-705-500a-3  
Perfect score: 1268  
Sequence: 1 MGNNAVLIVYISATHE.....NURGEDSPSHIKRSHESA 247

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 segs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seg length: 0  
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=cn1 -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blsum62 -TRANS=humat40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-DEF TIMEOUT=120 -MAMP TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*  
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3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/6CTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1268	100.0	771	2	US-09-361-736B-1
2	1268	100.0	771	2	US-09-193-881-2
3	1268	100.0	771	2	US-09-193-881-3
4	1268	100.0	771	2	US-09-193-881-4
5	1268	100.0	771	2	US-09-193-881-5
6	1268	100.0	771	2	US-09-193-881-6
7	1268	100.0	771	2	US-09-193-881-7
8	1268	100.0	771	2	US-09-193-881-8
9	1268	100.0	771	2	US-09-193-881-9
10	1268	100.0	771	2	US-09-193-881-10
11	1268	100.0	771	2	US-09-193-881-11
12	1268	100.0	771	2	US-09-193-881-12

13	352	27.8	892	4	US-09-361-736B-1	Sequence 1, Appl1
14	214	16.9	257	4	US-09-193-881-2	Sequence 2, Appl1
15	155	12.2	246	4	US-09-193-881-3	Sequence 3, Appl1
16	143.5	11.3	339	4	US-09-621-976-12801	Sequence 12801, A
17	98	7.7	285	4	US-09-193-881-1	Sequence 1, Appl1
18	93.5	7.4	3253	4	US-09-710-279-3955	Sequence 3955, Ap
19	93.5	7.4	30549	3	US-09-134-001C-322	Sequence 322, Ap
20	91	7.2	4348	4	US-09-828-062-5	Sequence 5, Appl1
21	90	7.1	1384	3	US-09-227-357-142	Sequence 142, Ap
22	86	6.8	1947	4	US-09-270-767-10718	Sequence 10718, A
23	86	6.8	1230025	4	US-09-198-452A-1	Sequence 1, Appl1
24	85.5	6.7	936	4	US-09-710-279-2459	Sequence 2459, Ap
25	85.5	6.7	1971	3	US-09-134-001C-1485	Sequence 1485, Ap
26	85.5	6.7	2818	4	US-09-710-279-3447	Sequence 3447, Ap
27	84	6.6	10136	4	US-08-353-700-2	Sequence 2, Appl1
28	84	6.6	10136	5	PCT-US95-16216-2	Sequence 2, Appl1
29	83.5	6.6	1000	4	US-09-655-908-7	Sequence 7, Appl1
30	83.5	6.6	1071	4	US-09-655-908-5	Sequence 5, Appl1
31	83.5	6.6	3084	4	US-09-762-724-7	Sequence 7, Appl1
32	83.5	6.6	3090	4	US-09-762-724-5	Sequence 5, Appl1
33	83	6.5	795	4	US-09-134-000C-2426	Sequence 2426, Ap
34	83	6.5	960	4	US-09-710-279-791	Sequence 791, Ap
35	83	6.5	960	4	US-09-710-279-2007	Sequence 2007, Ap
36	83	6.5	1197	4	US-09-710-279-43	Sequence 43, Appl1
37	83	6.5	1197	4	US-09-710-279-1497	Sequence 1497, Ap
38	83	6.5	1254	3	US-09-134-001C-973	Sequence 973, Ap
39	83	6.5	3264	4	US-09-710-279-4053	Sequence 4053, Ap
40	83	6.5	3314	4	US-09-710-279-3745	Sequence 3745, Ap
41	83	6.5	3314	4	US-09-710-279-3745	Sequence 3745, Ap
42	83	6.5	3393	4	US-09-710-279-4085	Sequence 4085, Ap
43	83	6.5	3885	4	US-09-710-279-3883	Sequence 3883, Ap
44	82	6.5	1089	3	US-09-134-001C-1833	Sequence 1833, Ap
45	82	6.5	4411529	3	US-09-103-840A-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-208-005C-1  
; Sequence 1, Application US/08208005C  
; Patent No. 5837498  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Copuscles of Stannius Protein, Stannocalcin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,005C  
; FILING DATE: 8 MARCH 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-78  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 1:  
; Sequence 1, Appl1



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Db      316 AACGGGTCACCTCCAGGTCCTTCCTCGCATTCGAGGTGCTCCACTTCCAAAAGANG 375
Qy      121 TLaalagluValGInguGluCySerSerlyLeuAsnValCySerSerIleAlaIysArg 140
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Qy      141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db      436 AACCTGAAGCCATCACTGAGTGTGCTGACCTGCCAATCACTTCCAAACATCTAT 495
Qy      161 AsnArgLeuValArgSerLeuLeuGluCyAspGluAspThrValSerThrIleArgAsp 180
Db      496 AACAGACTTCCGAAAGCCCTGCTGATGTGATGATGAGACACAGCTCAGCAATCAGAGAC 555
Qy      181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      556 AGCTGTATGAGAAATTTGGGCTTAACATGCGACGCTCTTCCACATCTCTGACAGACAG 615
Qy      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
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Qy      221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
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Qy      241 ArgThrSerHisGluSerAla 247
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RESULT 3
US-08-431-117A-1
; Sequence 1, Application US/08431117A
; Patent No. 5994301
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GIUFFRAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,117A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8 MARCH 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA

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US-08-431-117A-1
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Pred. No.: 4,64e-163 Length: 771
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
D: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-08-431-117A-1 (1-771)
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Db      76 GCGGAGCGAAAGTCTGTGAGGCCCGGAAATCCGAGTGGCGGCCAAACTCAGCT 135
Qy      41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db      136 GAAGTGTTCGTGTGCTCAACAGTGTCTTACAGTCCGCTGCGGGCTTTGCATGCTG 195
Qy      61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db      196 GAAACTCCACCTGTGACACAGATGGAGTGTATGACATCTGTAAATCCTTCTGTACAGC 255
Qy      81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
Db      256 GCTGCTAAATTTGACACTCAGAGAAAGCAATTCCTCAAGAGACTTAAATGCAATGCC 315
Qy      101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db      316 AACGGGTGCACCTCCAGAGTCTTCTCGCCATTCGAGGTGCTCCACTTCCAAAGAGAT 375
Qy      121 TLaalagluValGInguGluCySerSerlyLeuAsnValCySerSerIleAlaIysArg 140
Db      376 ATTCGTAGGTGAGGAGAGTGTCTACAGCAAGCTGAATGTGTGACGATCGCAAGCGG 435
Qy      141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db      436 AACCTGAAGCCATCACTGAGTGTGCTGACCTGCCAATCACTTCCAAACATCTAT 495
Qy      161 AsnArgLeuValArgSerLeuLeuGluCyAspGluAspThrValSerThrIleArgAsp 180
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Qy      181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      556 AGCTGTATGAGAAATTTGGGCTTAACATGCGACGCTCTTCCACATCTCTGACAGACAG 615
Qy      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
Db      616 CACTGTGCCCAACACACCCACAGAGCTGACTTCAACAGAGACGACCAATGAGCCGAG 675
Qy      221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
Db      676 AAGCTGAAGTCTCTCTCAGAAACCTCCGAGGTGAGAGAGACTCTCTCCCAATCAAA 735
Qy      241 ArgThrSerHisGluSerAla 247
Db      736 CGCACATCCCATGAGAGTCCA 756

RESULT 4
US-09-023-655-1502
; Sequence 1502, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: COCKE, BENJAMIN G.
; APPLICANT: COCKE, BENJAMIN G.
; APPLICANT: SUSAN G. STUART
; APPLICANT: JEFFREY J. SEILHAMER
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

```

TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1502:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3757 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 9975297  
US-09-023-655-1502

Alignment Scores:  
Pred. No.: 6 47e-162 Length: 3757  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-705-500a-3 (1-247) x US-09-023-655-1502 (1-3757)

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DB 220 GCGGAGACGAAATACCTCTGTGAGCCCCAGGAAATCCCGAGCGCTCAAAATCAGGT 279  
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
DB 280 GAAGTGGTGTGCTCTCAACAGTCTCTACAGTGGCTGGCGGCTTTTCCATGCCCG 339  
QY 61 GluAsnSerThrCysAspThrAspGlyMetIYrAspIleCysLysSerPheLeuIYrSer 80  
DB 340 GAAAACTCCACCTGTGACAGATGGATGTATGACATCTGTAATCCTTCTTGTACGC 399  
QY 81 AlaAlaLysPheAspThrGlnGlyIYrAlaPheValLysGlnSerLeuLysCysIleAla 100  
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QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
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QY 121 IleAlaGluValGlnGlnGlyCysIYrSerLysLeuAsnValCysSerIleAlaLysArg 140  
DB 520 ATTGCTAGGTGACGAGAGAGTCTACAGCACTAAATGTGTGCGCAATCGCCAGCGG 579  
QY 141 AspProGluAlaIleThrGluValGlnLeuProAsnHisPheSerAsnArgIYrIYr 160  
DB 580 AACCTGAAACCATCACTGAGTGTGTCAGCTGCCCAATCATCTTCCAAAGATACTAT 639  
QY 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp 180  
DB 640 AACAGACTGTCCGAACCTGCTGGAATGTATGATGAAGACAGCTCAGCAATCAAGAG 699  
QY 181 SerLeuValGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
DB 700 AGCTGATGAGAAATTTGGGCTTAACATGCCAGCTCTTCCACATCTTCAGACAGAC 759  
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrGlnGluProGln 220  
DB 760 CACTGTCCCAACACACCCACGAGCTGACTTCAACAGAGAGCAGCAATGAGCCGACG 819  
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
DB 820 AAGCTGAAGTCTCTCTCAGAACTCTCCAGTGAAGAGACTCTCTCCCATCAATCA 879  
QY 241 ArgThrSerHisGlnSerAla 247  
DB 880 CGCACATCCCATGAGAGTCA 900

RESULT 5  
US-08-831-132-13  
Sequence 13, Application US/08831132  
Patent No. 6008322  
GENERAL INFORMATION:  
APPLICANT: Kuestner, Rolf E.  
APPLICANT: Conklin, Darrell C.  
APPLICANT: Lok, Si  
APPLICANT: Buddle, Michele  
APPLICANT: Downey, William  
TITLE OF INVENTION: STANNIOCALCIN-2  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/831,132  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitskiak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 96-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6678  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 888 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: sig\_peptide





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QY 27 ValSerPro-----ArgLysSerArgValAla 36
Db 82 ACCAACCCCTCCGAGAGTCCCAAGACAGAGCTCCGACAGAAAGCGCTGCTCCG 141
QY 37 GluAsnSerIleValValValArgCysLeuAsnSerIleValValGlyCysGlyAla 56
Db 142 CAGAACACAGCGGAGATCCAGCATCTTTGCTCAAGCCGGGAGCTGGGCTGTGTG 201
QY 57 PheAlaCysIleuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSer 76
Db 202 TTGAGAGTGTTCAGAAACAACCTCTTGGAATCCAGGGTTTCATGGAGTTTGCAAGAG 261
QY 77 PheLeuTyrSerIleAlaLysPheAspThrGlnGlyValAlaPheValLysGluSerLeu 96
Db 262 TTTCGTGACACACCTGGAAATTCATGCCAGGAAAGTCAATTCATCAAGATGCTG 321
QY 97 LysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThr 116
Db 322 AGGTGCAAGGCCCATGCGCTGCTCAATTAATTTGCGTCGATCAGCAGAAATGTCAGCA 381
QY 117 PheGluArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSer 136
Db 382 ATTAGGAATGTGTTTCCAGTTGCAAGAGGAATGCTATCTGAAGCATGATGCTGCTCC 441
QY 137 IleAlaLysArgAsnProGluAlaIleThrGluValAlaGlnLeuProAsnHisPheSer 156
Db 442 GCAGCCAGAGAGAACTCGGTGATTTGGAGATATTCATTTCAGAGATCTCCGCTG 501
QY 157 AsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSer 176
Db 502 CATGAGCCCTATGTGACCTTGGAACCTGCTGCTCACTGCGGGGAATGTGAAGAG 561
QY 177 ThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIle 196
Db 562 GCAGTACCCGCGAGCTCCAGGCTCAGTGTGAACAGAGCTGGGAGAGCTCTGCTCCATC 621
QY 197 Leu-----GlnThrAspHisCysAlaGlnThrHis----- 206
Db 622 CTGAGTTTCTGCACCTCCATATATACAGACCTCCCAAGCGAGCCCAAGAGCATCAGCCC 681
QY 207 -----ProArgIleAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysVal 224
Db 682 CTGGCAGACAGGCTCAGCTCTCCAGGCTCACCACCGGAGCAACAACATCACTACACA 741
QY 225 LeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys----- 240
Db 742 GCCAAGCAGAGTCCAGAGGTGAGCGAGGAGCAAAAGCCACCGAATGCCATGCTCGA 801
QY 241 ---ArgThrSerHisGluSerAla 247
Db 802 GGCAGAAACGGTGGCCAGAGCGCT 825

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,132
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..72
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 73..906
FEATURE:
NAME/KEY: CDS
LOCATION: 1..906
US-08-831-132-1
Alignment Scores:
Pred. No.: 3,056-38 Length: 906
Score: 354.00 Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92% Indels: 12
DB: Gaps: 4
US-09-705-500A-3 (1-247) x US-08-831-132-1 (1-906)
QY 9 LeuValLeuValIleSer-----AlaSerAlaThrHisGluAla 21
Db 34 CTGGCTTTGGTGGTGGCCACCTTTGACCCCGGGGAGACCGACGCCAACCAACCC 93
QY 22 Glu---GluAsnAspSerValSerProArgLysSerArgValAlaAlaGluAsnSerAla 40
Db 94 GAGGATCCCAAGACAGAGAGCTCCAGCAGAAAGCCGCTGCTCCGCAAGATACAGCG 153
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 154 GAGATCCAGACCTGTTTGTCAACGCTGGCAGATGGGGTGGGCTGTTGAATGTTTC 213
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 214 GAGAACAACTCTTGTGAGATTCGGGGCTTACATGGGATTTGCATGACTTTTTCGACAC 273
QY 81 AlaAlaLysPheAspThrGlnGlyLysValAlaPheValLysGluSerLeuLysCysIleAla 100
Db 274 GCTGGAATAATTGATGTCAGGAGGCAAGTCAATCAAAACCCCTTGAATGTAAAGCC 333
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 334 CACCTCTGGCGCACAGATTCGCTGATAGCCGGAAGTCCCGGCATCAGAGGAATG 393
QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 394 GTGTCCAGTTGACGCGGGAATGTCACTCCACACAGACCTGTGCGCGCTGCCAGAG 453
QY 141 AspProGluAlaIleThrGluValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 454 AACACCCGGGTGATGTGAGATGATCATTTCAAGAGACTTGTCTGCTGCACGAACCTTAC 513

```

RESULT 7  
 US-08-831-132-1  
 Sequence 1, Application US/08831132  
 Patent No. 6088322  
 GENERAL INFORMATION:  
 APPLICANT: Kuestner, Rolf E.  
 APPLICANT: Conklin, Darrell C.  
 APPLICANT: Lok, Si  
 APPLICANT: Biddle, Michele  
 APPLICANT: Downey, William  
 TITLE OR INVENTION: STANNICOLALCIN-2  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk



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; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: human
US-09-361-736B-11

Alignment Scores:
Pred. No.: 3,74e-38      Length: 1024
Score: 354.00           Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92%      Indels: 12
DB: 4                   Gaps: 4

US-09-705-500a-3 (1-247) x US-09-361-736B-11 (1-1024)

QY 9 LeuValIeuValIleSer-----AlaSerAlaThrHisGluAla 21
DB 109 CTGGCTTTGGTGTGGCCACCTTTGACCCGGCGGGGAGACCGACGCCACCAACCCACC 168
QY 22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB 169 GAGGGTCCCCAAGACAGAGAGCTCCACAGAAAGCGCGCTGTCTCCGAGAAATACAGCG 228
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB 229 GAGATCCAGACAGCTGTGGTGCACAGCTGGCGGATGTGGGGTGGCGCTGTGAATGTTTC 288
QY 61 GlnAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLeuSerPheLeuTyrSer 80
DB 289 GAGAACACCTCTTGAGATTCGGGGCTTACATGGAATTTGATGACTTTTCTGCACAC 348
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
DB 349 GCTGGAAATTTGATATCCACAGGCGCAAGTCATTCATCAAGACGCTTGAATGTAAAGCC 408
QY 101 AsnGlyValIleThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB 409 CAGCTCTGGCGACAGGTTCCGCTCATAGCCCGGAAGTCCCGCCATCCAGGAATG 468
QY 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB 469 GTGTCCAGATTCAGCGGAGATCTCTACCAAGCAGACCTGTGCGCGCTCCACAGAG 528
QY 141 AspProGluAlaIleThrGluValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
DB 529 AACACCCGGGTGATGATGATGATGATTCATTCAGAGACTTGTCTGCACAGACCTTC 588
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
DB 589 GTGACCTCGTGAATTGCTGCTGACCTGTGGGAGAGAGTGAAGAGGCCATTCACCCAC 648
QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB 649 AGCGTCCAGGTTAGTGAAGCAGAACTGGGAGAGCTGTGCTCCATCTTG-----AGC 702
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
DB 703 TTCTGACCTCGGC-CATCCAGAGCTCCACAGCGGCCCGCCGAGCGCCACCCCAAGT 761
QY 221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluLysAspSerPro 236
DB 762 GGACAGAACCAAGCTCTCCAGGCGCCACACCGGGGAGAGAGACATCACT 812

RESULT 10
US-09-193-881-11
; Sequence 11, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen

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; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Kiass
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: 6248-US-91
; CURRENT APPLICATION NUMBER: US/09/193,881A
; CURRENT FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-881-11

Alignment Scores:
Pred. No.: 9.17e-38      Length: 1756
Score: 354.00           Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92%      Indels: 12
DB: 4                   Gaps: 4

US-09-705-500a-3 (1-247) x US-09-193-881-11 (1-1756)

QY 9 LeuValIeuValIleSer-----AlaSerAlaThrHisGluAla 21
DB 102 CTGGCTTTGGTGTGGCCACCTTTGACCCGGCGGGGAGACCGACGCCACCAACCCACC 161
QY 22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB 162 GAGGGTCCCCAAGACAGAGAGCTCCACAGAAAGCGCGCTGTCTCCGAGAAATACAGCG 221
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB 222 GAGATCCAGACAGCTGTGGTGCACAGCTGGCGGATGTGGGGTGGCGCTGTGAATGTTTC 281
QY 61 GlnAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB 282 GAGAACACCTCTTGAGATTCGGGGCTTACATGGAATTTGATGACTTTTCTGCACAC 341
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
DB 342 GCTGGAAATTTGATATCCACAGGCGCAAGTCATTCATCAAGACGCTTGAATGTAAAGCC 401
QY 101 AsnGlyValIleThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB 402 CAGCTCTGGCGACAGGTTCCGCTCATAGCCCGGAAGTCCCGCCATCCAGGGAATG 461
QY 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB 462 GTGTCCAGATTCAGCGGAGATCTCTACCAAGCAGACCTGTGCGCGCTCCACAGAG 521
QY 141 AspProGluAlaIleThrGluValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
DB 522 AACACCCGGGTGATGATGATGATGATTCATTCAGAGACTTGTGCTGCAGAACCTTAC 581
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
DB 582 GTGACCTCGTGAATTGCTGCTGACCTGTGGGAGAGAGTGAAGAGGCCATTCACCCAC 641
QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB 642 AGCGTCCAGGTTAGTGAAGCAGAACTGGGAGAGCTGTGCTCCATCTTG-----AGC 695
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
DB 696 TTCTGACCTCGGC-CATCCAGAGCTCCACAGGCGGCCCGCCGAGCGCCACCCCAAGT 754

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QY      221 LysLeuValLeuLeuArgAsn---LeuArgGlyGluGluAspSerPro 236
DB      755 GGACAGAACCAAGCTCTCCAGGGCCACCAAGGAGGAGGACATCACCCT 805

RESULT 11
US-09-193-881-10
; Sequence 10, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klass
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroppe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: 6248.US.P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; NUMBER OF SEQ. ID NOS: 29
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-881-10

Alignment Scores:
Pred. No.:      9.21e-38      Length:      1760
Score:          354.00      Matches:      82
Percent Similarity: 52.32%      Conservative: 42
Best Local Similarity: 34.60%      Mismatches: 102
Query Match:    27.92%      Indels:      12
DB:             4          Gaps:      4

US-09-705-500a-3 (1-247) x US-09-193-881-10 (1-1760)

QY      9 LeuValLeuValIleSer-----AlaSerAlaThrHisGluAla 21
DB      105 CTGGCTTGGTGTGGTGGACCTTTGACCGCGCGGGGAGACCGACCCACCAACCCACC 164

QY      22 Gln---GlnAsnAspSerValSerProAlaGlySerArgValAlaAlaGlnAsnSerAla 40
DB      165 GAGGGTCCCGACAGAGAGAGCTCCAGCAAGAAAGCGCGCTGCTCGACAGATACAGCG 224

QY      41 GlnValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCysLeu 60
DB      225 GAGATCCAGACTGTTTGGTCAACGCTGGCGAGATGGGCTGTGGCTGTTGAATCTTTC 284

QY      61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB      285 GAGACAACTCTGTGAGATTGGGGCTTACATGATTTGCATGACTTTTCGACCAAC 344

QY      81 AlaAlaLysPheAspThrGlnGlyValPheValAlaPheValGluSerLeuTyrCysIleAla 100
DB      345 GCTGGAAAATTTATAGCCAGGGGAGAGTCACTTCAAAAGACGCTTGAAATGTAAAGGCC 404

QY      101 AsnGlyValThrSerIleValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB      405 CAGGCTCTGGGACAGAGTTCCGCTCGCATTAAGCCGGAAGTCCCGGCCCATCGAGGAATG 464

QY      121 IleAlaGlnValGlnGlnGluCysTyrSerIleAsnValCysSerIleAlaLysArg 140
DB      465 GTGTCCCAAGTTGACGGGGAATGCTACCTCAAGCAAGACTGTGGCCGGCTCCCAAGAG 524

QY      141 AspProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
DB      525 AACACCCCGGTATATGAGGATGATGCATTTCAAGAGACTGTGTGTGACGACCAACCTTAC 584

QY      161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180

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DB      585 GTGACCTCGGTGACCTTCTGCTGACCTGTGGGAGAGAGGTGAAGAGCCATCACCCAC 644
QY      181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB      645 AGCTGCGAGCTTTCAGTGTGAGACAGACTGGGGAAGCTGTGCTCATCTTG-----AGC 698
QY      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgTyrThrAsnGluProGln 220
DB      699 TTCTGACCTGGGC-CATCCAGAGCTTCCACAGCGCGCCCCCGCCAGGCCACCCACAGT 757

QY      221 LysLeuValLeuLeuArgAsn---LeuArgGlyGluGluAspSerPro 236
DB      758 GGACAGAACCAAGCTCTCCAGGGCCACCAAGGAGGAGGACATCACCCT 808

RESULT 12
US-08-460-529B-1
; Sequence 1, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human stemlocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,529B
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13206
; FILING DATE: 10 NOV 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 892 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-08-460-529B-1

Alignment Scores:
Pred. No.:      5.57e-38      Length:      892
Score:          352.00      Matches:      81
Percent Similarity: 52.94%      Conservative: 45
Best Local Similarity: 34.03%      Mismatches: 101
Query Match:    27.76%      Indels:      12
DB:             2          Gaps:      4

US-09-705-500a-3 (1-247) x US-08-460-529B-1 (1-892)

QY      9 LeuValLeuValIleSer-----AlaSerAlaThrHisGluAla 21
DB      115 CTGGCTTGGTGTGGTGGACCTTTGACCGCGCGGGGAGACCGACGACCAACCAACCCACC 174

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```
QY 22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 175 GAGGATCCCAAGACAGAGAGCTCCACAGCAAGAGCCGCTGCTCCCTGAGAAATACAGG 234
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 235 GAGATCCAGACAGCTTTGGTCAACGCTGCGAGATGTGGGGTGTGGCTGTTCATTAAGTTTC 294
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 295 GAGAACAACTCTTGATGAGATTCGGGGCTTACATGCGATTTGATGACTTTTTCGACAAAC 354
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
Db 355 GCTGAAAATTGATTCGCCAGGCGCAAGTCATTCATCAAGACGCTTGAATGTAAGGCC 414
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 415 CACGCTCTGGGACAGGTTTCGGCTGCATTAAGCCGGAAGTCCCGGCTCATCGAGGAATG 474
QY 121 IleAlaGlnValGlnGlnGlnCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 475 GTGTCCAGTTGAGGGGAGATCTACCTCAAGACAGACCTGTGGCGGCTGCCAGAGAG 534
QY 141 AsnProGlnAlaIleThrGlnValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 535 AACACCCGGGTGATGTGAGATGATTCATTCACAGACTTGTCTGACACACACCTAC 594
QY 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180
Db 595 GTGACACTCTGTAACCTTGCTGACCTGTGGGAGAGAGTGAAGAGGCCATCACCCAC 654
QY 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 655 AGCGTGAGGTTGAGTGAGAGCAAGCTGGGGAAGCTGTGCTCCATCTTG-----AGC 708
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
Db 709 TTTCGACCTCGGA-CATCCAGAAAGCTCCACAGCGCCCGCCGAGCCAGCCAGGT 767
QY 221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGlnGlnAspSerProSer 237
Db 768 GACAGAACCAAGCTCTCCAGGCGCCACACCGGGGAGAGAGACATCACCTCC 821

RESULT 13
US-09-361-736B-1
; Sequence 1, Application US/09361736B
; Patent No. 661877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stannocalcin-Alpha
; FILE REFERENCE: PRI43PDI1
; CURRENT APPLICATION NUMBER: US/09361,736B
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 892
; TYPE: DNA
; ORGANISM: human
US-09-361-736B-1

Alignment Scores:
Pred. No.: 5,57e-38 Length: 892
Score: 352.00 Matches: 81
Percent Similarity: 52.94% Conservative: 45
Best Local Similarity: 34.03% Mismatches: 101
Query Match: 27,76% Indels: 12
DB: 4 Gaps: 4
```

```
US-09-705-500A-3 (1-247) X US-09-361-736B-1 (1-892)
QY 9 LeuValLeuValIleSer-----AlaSerAlaThrHisGlnAla 21
Db 115 CTGGCTTTGGTTGGTGGACCTTTGACCCGCGGGGAGCCAGCAGCACCAACCCACC 174
QY 22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 175 GAGGATCCCAAGACAGAGAGCTCCACAGCAAGAGCCGCTGCTCCCTGAGAAATACAGG 234
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 235 GAGATCCAGACAGCTTTGGTCAACGCTGCGAGATGTGGGGTGTGGCTGTTCATTAAGTTTC 294
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 295 GAGAACAACTCTTGATGAGATTCGGGGCTTACATGCGATTTGATGACTTTTTCGACAAAC 354
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
Db 355 GCTGAAAATTGATTCGCCAGGCGCAAGTCATTCATCAAGACGCTTGAATGTAAGGCC 414
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 415 CACGCTCTGGGACAGGTTTCGGCTGCATTAAGCCGGAAGTCCCGGCTCATCGAGGAATG 474
QY 121 IleAlaGlnValGlnGlnGlnCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 475 GTGTCCAGTTGAGGGGAGATCTACCTCAAGACAGACCTGTGGCGGCTGCCAGAGAG 534
QY 141 AsnProGlnAlaIleThrGlnValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 535 AACACCCGGGTGATGTGAGATGATTCATTCACAGACTTGTCTGACACACACCTAC 594
QY 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180
Db 595 GTGACACTCTGTAACCTTGCTGACCTGTGGGAGAGAGTGAAGAGGCCATCACCCAC 654
QY 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 655 AGCGTGAGGTTGAGTGAGAGCAAGCTGGGGAAGCTGTGCTCCATCTTG-----AGC 708
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
Db 709 TTTCGACCTCGGA-CATCCAGAAAGCTCCACAGCGCCCGCCGAGCCAGCCAGGT 767
QY 221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGlnGlnAspSerProSer 237
Db 768 GACAGAACCAAGCTCTCCAGGCGCCACACCGGGGAGAGAGACATCACCTCC 821

RESULT 14
US-09-193-881-2
; Sequence 2, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klass
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: 6248 US P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 257
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-881-2

Alignment Scores:
Pred. No.: 4.73e-20 Length: 257
Score: 214.00 Matches: 34
Percent Similarity: 69.41% Conservative: 25
Best Local Similarity: 40.00% Mismatches: 26
Query Match: 16.88% Indels: 0
DB: 4 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-193-881-2 (1-257)

QY 57 PheAlCysLeuGIuAsnSerThrCysAspThrAspGIyMetTyraSpIleCysIysSer 76
Db 2 TTGGATGCTTCCAGAAACAACCTCTGTGAGATCCGGGCTTACATGGATTTCCATGACT 61

QY 77 PheLeuTySerAlaAlaIysPheAspThrGIyLysAlaPheValIysGluSerLeu 96
Db 62 TTCTGCACAACCGCTGGAATTTGATGCCACGGCAAGTCATCAAAAGACGCTTG 121

QY 97 LysCysrIleAlaAngIyValThrSerIysValPheLeuAlaIleArgArgCysSerThr 116
Db 122 AAATGTAAAGCGCCACGCTCGCGCACAGCTTGCGCTCAATAGCCGAAAGTCCCGGCC 181

QY 117 PheGIArgMetIleAlaGIuValGIuGIyCysTySerIysLeuAsnValCysSer 136
Db 182 ATCAGGGAATGTCCTCCAGCTTGTCAGCGGGAATGCTCAAGCAGCAGCCTGTGCGG 241

QY 137 IleAlaIysArgAsn 141
Db 242 GCTGCCAGGAGAAC 256

RESULT 15
US-09-193-881-3
; Sequence 3, Application US/09193881A
; Patent No. 653819
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klass
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: 6248 US, P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-881-3

Alignment Scores:
Pred. No.: 4.93e-12 Length: 246
Score: 155.00 Matches: 27
Percent Similarity: 62.67% Conservative: 20
Best Local Similarity: 36.00% Mismatches: 24
Query Match: 12.22% Indels: 4
DB: 4 Gaps: 1

US-09-705-500A-3 (1-247) x US-09-193-881-3 (1-246)

QY 83 LysPheAspThrGIuGIyLysAlaPheValIysGluSerLeuIysCysIleAlaAngIy 102
Db 6 AAATTTATGCCCGGCAAGCTCATATCAAAAGACCGCTTGAATGTAAAGCCCAAGCT 65
```

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QY 103 ValThrSerIysValPheLeuAlaIleArgArgCysSerThrPheGIArgMetIleAla 122
Db 66 CTGCCGCACAGGTTCCGCTGCATAGCCGGAAGTCCCGGCCATCAGGAAATGTGTCC 125

QY 123 GIuValGIuGIuGIyCysTySerIysLeuAsnValCysSerIleAlaIysArgAsnPro 142
Db 126 CAGTTGCACCGCGGAATGCTACCTCAAGCAGCAGCCTGTGCCGCTGCCAGAGAACACC 185

QY 143 GIuAlaIleThrGIuValIleGIuLeuProAsnHisPheSerAsn 157
Db 186 CCGGTGATAGTGAATGATC-----CATTTCAAGAAC 218

Search completed: November 22, 2004, 18:13:35
Job time : 129 secs
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 22, 2004, 18:09:53 ; Search time 524 Seconds

(without alignments)  
2547.128 Million cell updates/sec

Title: US-09-705-500A-3  
Perfect score: 1268  
Sequence: 1 MGNASAVLVLTASATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table:  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 362788 segs, 2701811610 residues  
Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-TRANS-human40.ccl -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
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Database: Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	771	US-10-416-05T-1	Sequence 1, Appl1
2	1268	100.0	1283	US-09-844-989A-1	Sequence 1, Appl1
3	1268	100.0	1283	US-10-614-990A-1	Sequence 1, Appl1
4	1268	100.0	3757	US-10-641-642-1582	Sequence 1502, Ap
5	1268	100.0	3756	US-10-044-090-638	Sequence 638, Ap
6	1268	100.0	3897	US-10-198-845-13651	Sequence 13651, A
7	1268	100.0	3901	US-10-177-253-470	Sequence 440, App
8	1268	100.0	3901	US-10-465-524-127	Sequence 17, Appl
9	1268	100.0	3901	US-10-159-569-292	Sequence 292, App
10	1268	100.0	3901	US-10-372-683-410	Sequence 40, Appl
11	1268	100.0	3901	US-10-240-925-1425	Sequence 1425, Ap
12	1250	98.6	2572	US-09-925-906-486	Sequence 486, App
13	861	67.9	585	US-09-778-320-149	Sequence 149, App
14	861	67.9	585	US-09-910-689-149	Sequence 149, App
15	861	67.9	585	US-10-010-742-149	Sequence 149, App
16	861	67.9	585	US-10-714-389-149	Sequence 149, App
17	861	67.9	585	US-10-717-296-149	Sequence 149, App
18	689	54.3	473	US-10-060-036-2677	Sequence 2677, Ap
19	508	40.1	420	US-09-778-320-141	Sequence 141, App
20	508	40.1	420	US-09-910-689-141	Sequence 141, App
21	508	40.1	420	US-10-010-742-141	Sequence 141, App
22	508	40.1	420	US-10-714-389-141	Sequence 141, App
23	508	40.1	420	US-10-717-296-141	Sequence 141, App
24	396	31.2	436	US-09-918-595-33032	Sequence 33032, A
25	380	30.0	560	US-10-029-386-9487	Sequence 9487, Ap
26	370	28.2	219	US-09-864-761-21309	Sequence 21309, A
27	363	28.6	215	US-10-029-386-23167	Sequence 23167, A
28	354	27.9	1024	US-10-418-226-1	Sequence 11, Appl
29	354	27.9	1756	US-09-193-881-11	Sequence 11, Appl
30	354	27.9	1756	US-10-338-395-11	Sequence 11, Appl
31	354	27.9	1760	US-09-193-881-10	Sequence 10, Appl
32	354	27.9	1760	US-10-338-395-10	Sequence 10, Appl
33	354	27.9	1837	US-10-364-889-3	Sequence 3, Appl1
34	354	27.9	1837	US-10-058-270A-21	Sequence 21, Appl
35	354	27.9	2380	US-09-918-624B-54	Sequence 54, Appl
36	354	27.9	2380	US-10-172-118-946	Sequence 442, App
37	354	27.9	2380	US-10-172-118-946	Sequence 946, App
38	354	27.9	2380	US-10-295-027-99	Sequence 99, Appl
39	354	27.9	2380	US-10-173-999-79	Sequence 79, Appl
40	354	27.9	2380	US-10-159-563-109	Sequence 109, App
41	354	27.9	2380	US-10-382-887-946	Sequence 946, App
42	354	27.9	2759	US-10-198-846-9993	Sequence 9993, App
43	354	27.9	4173	US-10-071-766-128	Sequence 128, App
44	352	27.8	892	US-09-361-736-1	Sequence 1, Appl1
45	352	27.8	892	US-10-418-226-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-10-116-051-1  
; Sequence 1, Application US/10116051  
; Publication No. US20020146791A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: COMPOSABLES OF STANNIUS PROTEIN, STANNIICALCIN  
; FILE REFERENCE: PF108PID1C1  
; CURRENT APPLICATION NUMBER: US/10/116\_051  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/312,610  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 08/431,117  
; PRIOR FILING DATE: 1995-04-28  
; PRIOR APPLICATION NUMBER: 08/208,005  
; PRIOR FILING DATE: 1994-03-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 771  
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-116-051-1

Alignment Scores:
Pred. No.: 7.23e-166 Length: 771
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-705-500a-3 (1-247) x US-10-116-051-1 (1-771)

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QY 21 AlAGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 76 GCGGAGCAGAAATGATCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAACTCAGCT 135
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValIGlyCysGlyValAlaPheAlaCysLeu 60
Db 136 GAAAGTGTCTGCTGCTCCAAACAGTCTTACAGTGGCTGGCGGCTTTTGCATGCTG 195
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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QY 81 AlaAlaLysPheAspThrGlnGlyValAlaPheValLysGlnSerLeuLysCysIleAla 100
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QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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; Sequence 1, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stannicalcain Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
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; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(788)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (857)..(857)
; OTHER INFORMATION: n is equal to a, t, c, or g.
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; US-09-840-989A-1

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Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Db 45 ATGCTCCAAACCTCAGAGAGCTTCTGCTGCTGATGATGCTTCTCCAAACCATGAG 104
QY 21 AlAGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
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Db 165 GAAAGTGTCTGCTGCTCCAAACAGTCTTACAGTGGCTGGCGGCTTTTGCATGCTG 224
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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; Sequence 1, Application US/10614990  
; Publication No. US20040198658A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based Th  
; FILE REFERENCE: PFI08P2  
; CURRENT APPLICATION NUMBER: US/10/614,990  
; CURRENT FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: US/09/840,989A  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/29432  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,740  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1283  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (45)..(788)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (857)..(857)  
; OTHER INFORMATION: n is equal to a, t, c, or g.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1254)..(1254)  
; OTHER INFORMATION: n is equal to a, t, c, or g.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1279)..(1279)  
; OTHER INFORMATION: n is equal to a, t, c, or g.  
US-10-614-990-1  
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Pred. No. 1,7e-165 Length: 1283  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-09-705-500a-3 (1-247) x US-10-614-990-1 (1-1283)  
QY 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20  
DB 45 ATGCTCCAAAATCAGCAGTCTTCTGAGTCTGATGATGCTCTTCTGCAACCCATGAG 104  
QY 21 AlGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40  
DB 105 GCGAGACGAATGACTCTGTGAGCCCGCAGAAATCCCGAGTGGCGGCCAAATCAGCT 164

QY 41 GluValAlaArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
DB 165 GAAGGTGTTCTTGGCTTCAACAGTGCTCTTACAGGTGGCTTGGAGGCTTTTGACATGGCTG 224  
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
DB 225 GAAATCTCACCTGTGACACAGATGGATGTATATCATCTTAATCTTCTTGTACAGC 284  
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100  
DB 285 GCTGCTAAATTTGACACTCAGAGAAAGCATCTCTCAAGAGACCTTAATAATGATGATGCC 344  
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
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QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
DB 405 ATTGCTGAGTGACAGAAAGATGTCTACAGCAAGCTGATGTGTGACATGCGCAAGCGG 464  
QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
DB 465 AACCTGAAGCCATCAGAGAGTGTCTCCAGCTGCCCATCTCTCCAAACGATATCAT 524  
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180  
DB 525 AAGACACTTGTCCGAAGCTCTGTGAATGTATGAAGACACAGTCAGACATCAGAGAC 584  
QY 181 SerLeuMetGluValIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
DB 585 AGCGTGAAGAGAAATGGGCTTAACATGGCCAGCTCTTCCACATCCCTGCAGACGAC 644  
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220  
DB 645 CACTGTGCCAAACACACCCAGAGCTGACTTCAACAGGAGACGACCAATGAGCCGCGAG 704  
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
DB 705 AAGCTGAAGTCTCTCCACAGAACTCCGAGTGAGAGAGACTCTCCCTCCACATCAAA 764  
QY 241 ArgThrSerHisGluSerAla 247  
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RESULT 4  
US-10-641-643-1502  
; Sequence 1502, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>  
Filing Date: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1502:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3757 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 975297  
SEQUENCE DESCRIPTION: SEQ ID NO: 1502 :  
US-10-641-643-1502  
Alignment Scores:  
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Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
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DB 280 GAAGTGGTGGTGGCTCCACAGTGTCTTACAGTGGCTGGCGGAGCTTTTGATGCCG 339  
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DB 340 GAAATCTCCACCTGTGACAGATGGAGATGATGACATCTGTAATCTCTTTGTRACG 399  
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QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
DB 520 ATTGCTAGAGTGAAGAGAGAGTCTCTACGCAACTGATGTCAGCATCGCAAGCGG 579  
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DB 700 AGCTGTATGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTTCGACAGACAG 759  
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220

DB 760 CACTGTGCCAAACACACCCAGAGCTGACTTCAACAGAGACCAATGAGCCGAG 819  
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluLysAspSerProSerHisIleLys 240  
DB 820 AAGCTGAAGTCTCTCTCCAGGAACCTCGAGGTGAGAGAGACTCTCCCTCCACATCAA 879  
QY 241 ArgThrSerHisGluSerAla 247  
DB 880 CGCACATCCCATGAGAGTGA 500  
RESULT 5  
US-10-044-090-638  
Sequence 638, Application US/10044090  
Publication No. US20020137081A1  
GENERAL INFORMATION:  
APPLICANT: Olga Bandman  
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
FILE REFERENCE: PA-0028 US  
CURRENT APPLICATION NUMBER: US/10/044,090  
NUMBER OF SEQ ID NOS: 850  
CURRENT FILING DATE: 2002-01-09  
SOFTWARE: PERL Program  
SEQ ID NO 638  
LENGTH: 3765  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No. US20020137081A1 331181.1  
NAME/KEY: unsure  
LOCATION: 2378, 3184, 3187, 3194  
OTHER INFORMATION: a, t, c, g, or other  
US-10-044-090-638  
Alignment Scores:  
Pred. No.: 1,04e-164 Length: 3765  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 13  
US-09-705-500a-3 (1-247) x US-10-044-090-638 (1-3765)  
QY 1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20  
DB 174 ATGCTCCAAAACACAGAGAGCTTCGTGCTGATATGATGCTTCTCAACCCATGAG 223  
QY 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40  
DB 234 GCGGAGCAAGATGACTCTGTGAGCCCGAGGAATCCCGAGTGGCGCTCAAACTAGCT 293  
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
DB 294 GAAGTGGTGGTGGCTCCACAGTGTCTTACAGTGGCTGGCGGAGCTTTTGATGCCG 353  
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
DB 354 GAAATCTCCACCTGTGACAGATGGAGATGATGACATCTGTAATCTCTTTGTRACG 413  
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100  
DB 414 GCTGCTAAATTTGACACTCGGGAAGACATTCGTCAAGAGAGCTTAAATGCAATCGCC 473  
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
DB 474 AACGGGGTCACTCCCAAGGCTTCTCGCCATTCGAGGAGTGTCCCACTTCCAAAGGATG 533  
QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
DB 534 ATTGCTAGAGTGAAGAGAGTGTCTTACGCAACTGATGTCAGCATCGCAAGCGG 593  
QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160

DB 594 AACCTGGAACCATCTGAGTGCCTCCAGCTCCCAATCATCTTCCCAACGATCTAT 653  
 QY 161 AAsArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180  
 DB 654 AACGACCTTCCGAAGCCCTGCTGGAATGTGATGAAAGACACAGTCAACATCAAGAC 713  
 QY 181 SerLeuMetGluValIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
 DB 714 AGCCTGATGAGAAATTGGGCTTAACATGCGCAGCCTCTCCACATCTCCGACAGACAG 773  
 QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220  
 DB 774 CACTGTGCCAAACACACCCACGAGCTGACTTCAACAGGAGACGACCAATGAGCCGAG 833  
 QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleLys 240  
 DB 834 AAGGTAAATGCTCTCTCAGGAACCTCCGAGTGAGAGAGACTCTCCCTCCCACTCAAA 893  
 QY 241 ArgThrSerHisGluSerAla 247  
 DB 894 CGCACATCCCATGAGAGTGCA 914

## RESULT 6

US-10-198-846-13651  
 ; Sequence 13651, Application US/10198846  
 ; Publication No. US20030099974A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Xu, Yongyao  
 ; APPLICANT: Wang, Youzhen  
 ; APPLICANT: Steinmann, Kathleen  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; TITLE OF INVENTION: THERAPY OF BREAST CANCER  
 ; FILE REFERENCE: MRI-049  
 ; CURRENT APPLICATION NUMBER: US/10/198,846  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/306,220  
 ; PRIOR FILING DATE: 2001-07-18  
 ; NUMBER OF SEQ ID NOS: 14084  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 13651  
 ; LENGTH: 3897  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887,  
 ; LOCATION: 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-10-198-846-13651

## Alignment Scores:

Pred. No.: 1,1e-164 Length: 3897  
 Score: 1268.00 Matches: 247  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

US-09-705-500a-3 (1-247) x US-10-198-846-13651 (1-3897)

QY 1 MetLeuGlnAsnSerAlaValLeuLeuValIleSerAlaSerAlaThrHisGlu 20  
 DB 285 ATGCTCCAAACTAGACAGTCTCTCTGTGTGTATCATGTCTTTCACACCATGAG 344  
 QY 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgAlaAlaGlnAsnSerAla 40  
 DB 345 GCGAGAGGAAATGACTGTGTAGCCCAAGAAATCCGAGTGGCGGTCAAACTCAGCT 404  
 QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60

DB 405 GAGTGTGCTGCTGCTCAACAGTCTCTACAGTCCGCTCCGGGCTTTTGATGCTG 464  
 QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
 DB 465 GAAATCTCCACTGTGACACAGATGGGATGTATGACATCTGTAATCTCTTGTACAGC 524  
 QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100  
 DB 525 GCTGTAAATTGACACTCAGAGAAAGCATTCGTCAAGAGAGCTTAAATGATGCTCC 584  
 QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
 DB 585 AACGGGTCACTCCCAAGTCTCTGCTCCATTTGGAGGTGCTCACTTCCAAAGGATG 644  
 QY 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
 DB 645 ATTGCTGAGGTGCAGAGAGAGTGTACAGCAAGCTGAAATGTGCAGCATGCGAAGCG 704  
 QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
 DB 705 AACCTGAAGCCATCATCTGAGTCTCCAGTCCCAATCATCTTCCAAAGATCTAT 764  
 QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180  
 DB 765 AACGACTTGTCCGAAGCCTGCTGAATGTATGATGAAGACACAGTCAGCACATCAGAGAC 824  
 QY 181 SerLeuMetGluValIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
 DB 825 AGCCTGAGGAGAAATTTGGGCTTACATGAGCCAGCTCTTCCATCTTCCAGACAGAC 884  
 QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220  
 DB 885 CACTGTGCCAAACACACCCACGAGCTGACTTCAACAGAGACGACCAATGAGCCGAG 944  
 QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleLys 240  
 DB 945 AAGCTGAAGTCTCTCTCAGGAACCTCCGAGGTGAGAGAGCTCTCCCTCCCACTCAA 1004  
 QY 241 ArgThrSerHisGluSerAla 247  
 DB 1005 CGCACATCCCATGAGAGTGCA 1025

## RESULT 7

US-10-177-293-440  
 ; Sequence 440, Application US/10177293  
 ; Publication No. US20030124128A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Glatt, Karen  
 ; APPLICANT: Zhao, Xumei  
 ; APPLICANT: Gannavarpu, Manjula  
 ; APPLICANT: Kamatkar, Shubhangi  
 ; APPLICANT: Mertens, Maureen  
 ; APPLICANT: Myer, Vic  
 ; APPLICANT: Wang, Youzhen  
 ; APPLICANT: Xu, Yongyao  
 ; APPLICANT: Hoersch, Sebastian  
 ; APPLICANT: Monahan, John  
 ; APPLICANT: Meyers, Rachel E.  
 ; APPLICANT: Bast Jr., Robert C.  
 ; APPLICANT: Horrobagyl, Gabriel N.  
 ; APPLICANT: Fustai, Lajos  
 ; APPLICANT: Weric, Funda  
 ; APPLICANT: Sahin, Aysegul  
 ; APPLICANT: Mills, Gordon B.  
 ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
 ; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER  
 ; FILE REFERENCE: MRI-038  
 ; CURRENT APPLICATION NUMBER: US/10/177,293  
 ; PRIOR FILING DATE: 2002-06-21  
 ; PRIOR APPLICATION NUMBER: US 60/299,887  
 ; PRIOR FILING DATE: 2001-06-21  
 ; PRIOR APPLICATION NUMBER: US 60/301,572

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/ PRIOR FILING DATE: 2001-06-27
/ PRIOR APPLICATION NUMBER: US 60/306,501
/ PRIOR FILING DATE: 2001-07-18
/ PRIOR APPLICATION NUMBER: US 60/325,002
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: US 60/362,585
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/xxx,xxx
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 506
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 440
/ LENGTH: 3901
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-177-293-440

Alignment Scores:
Pred. No.: 1,1e-164 Length: 3901
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 15

US-09-705-500a-3 (1-247) x US-10-177-293-440 (1-3901)

QY 1 MetLeuGlnAnsSerAlaValLeuLeuValIleSerAlaSerAlaThrHisGlu 20
Db ATGCTCCAAAACCTCAGACAGTCTTCTGCTGATGATGCTTCTCCAACTCATGAG 344

QY 21 AlaGlnGlnAnsSerAlaSerProArgLysSerArgValAlaAlaGlnAnsSerAla 40
Db GCGGAGCAGATGATCTGTGAGCCCGAGAAATCCCGATGGCGGCTCAAACTCATG 404

QY 41 GluValValArgCysLeuAnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db GAAGTGGTGTGCTGCTCCCAACAGTCTCTACAGCTCGCGCTGGCGGCTTTGGATCG 464

QY 61 GluAnsSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db GAAACTCCACCTGTCACAGATGGAGATGTATGATCTGTAATCTCTTGTATCAGC 524

QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
Db GCTGCTAAATTTGACATCAGGAAAGCATTCGTCAAGAGAGCTTAATATGCATCGCC 584

QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db AACGGGCTCACCTCCCAAGGCTTCTCCGCAATCGAGAGTCCCATTTCCAAAGAGAG 644

QY 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAnsValCysSerIleAlaLysArg 140
Db ATTGCTGAGGTGACGAGAGAGTCTCTACGACGTAATGTGTGACGATCCGCAAGCG 704

QY 141 AsnProGlnAlaIleThrGluValValGlnLeuProAnsHisPheSerAsnArgTyr 160
Db AACCTCGAAGCCATCTCATGAGTGTCTCCAGCTGCCAATCATCTTCCCAACGATCAT 764

QY 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp 180
Db AACAGATTTCTCCGAAGCTCTGCTGAGATGTATGATGAACACAGTCAACATTCAGAG 824

QY 181 SerLeuMetGlnLysIleGlyProAnsMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db AGCTCATGAGAAATTTGGGCTTAACATGCGCAGCTCTTCACATCTTCGACAGACAG 884

QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
Db CACTGTGCCCAACACACCCACGAGCTGACTTAAAGAGAGAGCCCATATAGCGCGAG 944

QY 221 LysLeuLysValLeuLeuArgLeuAnsGlyGlnGluAspSerProSerHisIleLys 240
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Db 945 AAGCTGAAGTCTCTCCAGAACTCCGAGGTGAGAGGATCTCTCCCTCCACATCAAA 1004
QY 241 ArgThrSerHisGluSerAla 247
Db 1005 CGCAGATCCCATGAGATGCA 1025

RESULT 8
US-10-465-572-17
/ Sequence 17, Application US/10465572
/ Publication No. US20030207840A1
/ GENERAL INFORMATION:
/ APPLICANT: Riggs, Gregory
/ TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
/ FILE REFERENCE: 000250.00012
/ CURRENT APPLICATION NUMBER: US/10/465,572
/ CURRENT FILING DATE: 2003-06-20
/ PRIOR APPLICATION NUMBER: US/10/201,642
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/307,600
/ PRIOR FILING DATE: 2001-07-26
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 3901
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-465-572-17

Alignment Scores:
Pred. No.: 1,1e-164 Length: 3901
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 15

US-09-705-500a-3 (1-247) x US-10-465-572-17 (1-3901)

QY 1 MetLeuGlnAnsSerAlaValLeuLeuValIleSerAlaSerAlaThrHisGlu 20
Db ATGCTCCAAAACCTCAGACAGTCTTCTGCTGATGATGCTTCTCCAACTCATGAG 344

QY 21 AlaGlnGlnAnsSerAlaSerProArgLysSerArgValAlaAlaGlnAnsSerAla 40
Db GCGGAGCAGATGATCTGTGAGCCCGAGAAATCCCGATGGCGGCTCAAACTCATG 404

QY 41 GluValValArgCysLeuAnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db GAAGTGGTGTGCTGCTCCCAACAGTCTCTACAGCTCGCGCTGGCGGCTTTGGATCG 464

QY 61 GluAnsSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db GAAACTCCACCTGTCACAGATGGAGATGTATGATCTGTAATCTCTTGTATCAGC 524

QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
Db GCTGCTAAATTTGACATCAGGAAAGCATTCGTCAAGAGAGCTTAATATGCATCGCC 584

QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db AACGGGCTCACCTCCCAAGGCTTCTCCGCAATCGAGAGTCCCATTTCCAAAGAGAG 644

QY 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAnsValCysSerIleAlaLysArg 140
Db ATTGCTGAGGTGACGAGAGAGTCTCTACGACGTAATGTGTGACGATCCGCAAGCG 704

QY 141 AsnProGlnAlaIleThrGluValValGlnLeuProAnsHisPheSerAsnArgTyr 160
Db AACCTCGAAGCCATCTCATGAGTGTCTCCAGCTGCCAATCATCTTCCCAACGATCAT 764

QY 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp 180
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Db 765 AACGAGCTTGCCGAGCCTGCTGATGATGATGAGACAGACAGTACAGCAATCAGAGAC 824  
Qy 181 SerLeuMeGluLysIleGlyProAsnMeCAlaSerLeuPheHisIleLeuGlnThrAsp 200  
Db 825 AGCCTATGAGAAATTGGGCTTAACATGGCCAGCCTCTTCCACATCTCTGACAGACAGC 884  
Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220  
Db 885 CACTGTGCCCAACACACACCAGAGCTGACTTCAACAGAGAGCGACCAATGAGCCGAG 944  
Qy 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
Db 945 AACCTGAAAGTCTCTCTCCAGAACCTCCGAGTGAGAGAGACTCTCTCCACATCAAA 1004  
Qy 241 ArgThrSerHisGluSerAla 247  
Db 1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 9  
US-10-159-563-292  
; Sequence 292, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Melzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; FILE REFERENCE: 11613.55US11  
; CURRENT APPLICATION NUMBER: US/10/159,563  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 292  
; LENGTH: 3901  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-159-563-292

Alignment Scores:  
Pred. No.: 1,1e-164 Length: 3901  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-705-500A-3 (1-247) x US-10-159-563-292 (1-3901)

Qy 1 MetLeuGlnAsnSerAlaValLeuValIleSerAlaSerAlaThrHisGlu 20  
Db 285 ATGCTCCAAACTCAGCAGTGTCTGTGCTGTGATCATGCTCTTCTCAACCCATGAG 344  
Qy 21 AlAGluGlnAsnAspSerValSerProArgLysSerArgValAlaIaGlnAsnSerAla 40  
Db 345 GCGGAGCAGATATGACTCTGTGAGCCCCAGGAAATCCCGAGTGCGGCTCAAACTGAGCT 404  
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValaPheAlaCysLeu 60  
Db 405 GAGTGGTTTGTTGCTCCTCAACAGTGTCTACAGTGGGCTGGGGCTTTTGATGCTCG 464  
Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
Db 465 GAAAAACCCACCTGTGACACAGATGGGATATGACATCTGTAATCTTCTTGTCACGC 524  
Qy 81 AlAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100  
Db 525 GCTGCTAAATTGACATCTGAGGAGAAAGCATTTGTCAAAGAGGCTTAAATGATCATGCGC 584  
Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120

Db 585 AACGGGGACCTCCAAAGTCTTCTCCGCAATTCGAGGAGTGCTCACCTTCCAAAGATG 644  
Qy 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
Db 645 ATTGCTGAGTGAGGAGAAAGTGTCTACAGCAAGCTGATGTGTGACATGCGCAACCG 704  
Qy 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
Db 705 AACCTGAGCCATCATCTGAGTGTCTGACGTGCGCCATCATCTTCCAAACAGATCATAT 764  
Qy 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180  
Db 765 AACGACTTGCCGAGAGCTGCTGGAATGTGATGAACACAGTCAACACATCAGAGAC 824  
Qy 181 SerLeuMeGluLysIleGlyProAsnMeCAlaSerLeuPheHisIleLeuGlnThrAsp 200  
Db 825 AGCCTGATGAGAAATTGGGCTTAACATGGCCAGCCTCTTCCACATCTCTGACAGACAGC 884  
Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220  
Db 885 CACTGTGCCCAACACACACCAGAGCTGACTTCAACAGAGAGCGACCAATGAGCCGAG 944  
Qy 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
Db 945 AACCTGAAAGTCTCTCTCCAGAACCTCCGAGTGAGAGAGACTCTCTCCACATCAAA 1004  
Qy 241 ArgThrSerHisGluSerAla 247  
Db 1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 10  
US-10-372-683-40  
; Sequence 40, Application US/10372683  
; Publication No. US20040009171A1  
; GENERAL INFORMATION:  
; APPLICANT: GERRITSEN, MARY E.  
; APPLICANT: PEALE TR., FRANKLIN V.  
; APPLICANT: WU, THOMAS D.  
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA  
; FILE REFERENCE: P1928R1P1  
; CURRENT APPLICATION NUMBER: US/10/372,683  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 10/271,690  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US 60/344,534  
; PRIOR FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 40  
; LENGTH: 3901  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-372-683-40

Alignment Scores:  
Pred. No.: 1,1e-164 Length: 3901  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-705-500A-3 (1-247) x US-10-372-683-40 (1-3901)

Qy 1 MetLeuGlnAsnSerAlaValLeuValIleSerAlaSerAlaThrHisGlu 20  
Db 285 ATGCTCCAAACTCAGCAGTGTCTGTGCTGTGATCATGCTCTTCTCAACCCATGAG 344  
Qy 21 AlAGluGlnAsnAspSerValSerProArgLysSerArgValAlaIaGlnAsnSerAla 40  
Db 345 GCGGAGCAGATATGACTCTGTGAGCCCCAGGAAATCCCGAGTGCGGCTCAAACTGAGCT 404  
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValaPheAlaCysLeu 60

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Db      405 GAAGTGGTTCGTCCTCAACAGTCTCAACAGTCTCGGCTGGGGCTTTTGATGCTCG 464
Qy      61  GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db      465 GAAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAATCCCTCTTGACAC 524
Qy      81  AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
Db      525 GCTGCTAAATTTTACACTCGGAGAAAACATTTGTCMAAGAGAGCTTAAATGTCATCGCC 584
Qy      101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db      585 AAGGGGTGACCTCCAGAGCTCTTCCTCCGCAATCCGAGGTGCTCCACTTCCAAAGAGATG 644
Qy      121 AlaAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db      645 ATTGCTGAGGTGACGAGAGAGTCTTACAGCAAGCTTAATGTGACGATCCGCAAGCG 704
Qy      141 AsnProGluAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db      705 AACCTGAAAGCCACTGAGGTGCTCCAGCTCCCAATCACTTCCAAAGATCTAT 764
Qy      161 AsnArgLeuValArgSerLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db      765 AACAGACTGTCCGAAAGCTGTGAGATGTGAAGAACAGTCAAGCAATCAAGAGAC 824
Qy      181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      825 AGCTGATGAGAAATTTGGGCTTACATGGCCAGCTCTTCCACATCTTCAGACAGAC 884
Qy      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
Db      885 CACTGTGCCCAACACACACACAGAGTGAATCTTCAAGAGAGAGAGCCATATAGCCGACG 944
Qy      221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleLys 240
Db      945 AACCTGAAGTCTCTCTCAAGAACCTCCAGGTGAAGAGAGATCTCTCCCAATCAAA 1004
Qy      241 ArgThrSerHisGluSerAla 247
Db      1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 11
US-10-240-425-1425
; Sequence 1425, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Metzel, Jon C.
; APPLICANT: Scheff, Uwe
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1425
; LENGTH: 3901
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 U25997
US-10-240-425-1425

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Alignment Scores:
Pred. No.: 1,1e-164 Length: 3901
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Db: 16 Gaps: 0

US-09-705-500A-3 (1-247) X US-10-240-425-1425 (1-3901)
Qy      1  MetLeuGlnAsnSerAlaValLeuLeuValIleSerAlaSerAlaThrHisGlu 20
Db      285 ATGCTCCAAAATCAGACAGTGTCTGTGCTGTGATCACTGCTTCTTGCACACCATGAG 344
Qy      21  AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db      345 GCGAGAGAGATATGACTGTGTGAGGCCAGGAATCCGAGTGGCGGCTCAAACTAGCT 404
Qy      41  GluValValArgCysLeuAsnSerAlaLeuGlnValGlyGlyValAlaPheAlaCysLeu 60
Db      405 GAAGTGGTTCGTCCTCAACAGAGTCTTACAGTCCGCTGCGGGCTTTTGATGCTCG 464
Qy      61  GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db      465 GAAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAATCTTCTTGATCAGC 524
Qy      81  AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
Db      525 GCTGCTAAATTTTGAACCTCAAGGAGAAAGATTCGTCMAAGAGCTTAAATGTCATCGCC 584
Qy      101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db      585 AAGGGGTGACCTCCAGAGCTCTTCCTCCGCAATCCGAGGTGCTCCACTTCCAAAGATG 644
Qy      121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db      645 ATTGCTGAGGTGACGAGAGAGTCTTACAGCAAGCTTAATGTGACGATCCGCAAGCG 704
Qy      141 AsnProGluAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db      705 AACCTGAAGCCACTGAGAGTGTCTCAAGCTCCCAATCACTTCCCAAGATCTAT 764
Qy      161 AsnArgLeuValArgSerLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db      765 AACGAGACTGTCCGAAAGCTGTGAGATGTGAAGAACAGTCAAGCAATCAAGAGAC 824
Qy      181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      825 AGCTGATGAGAAATTTGGGCTTACATGGCCAGCTCTTCCACATCTTCAGACAGAC 884
Qy      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
Db      885 CACTGTGCCCAACACACACACAGAGTGAATCTTCAAGAGAGAGAGCCATATAGCCGACG 944
Qy      221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleLys 240
Db      945 AACCTGAAGTCTCTCTCAAGAACCTCCAGGTGAAGAGAGATCTCTCCCAATCAAA 1004
Qy      241 ArgThrSerHisGluSerAla 247
Db      1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 12
US-09-925-300-486
; Sequence 486, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Ruben,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10

```



PRIOR APPLICATION NUMBER: PCT/US00/05988  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: 60/124,270  
 PRIOR FILING DATE: 1999-03-12  
 NUMBER OF SEQ ID NOS: 1890  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 486  
 LENGTH: 2572  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURES:  
 NAME/KEY: misc feature  
 LOCATION: (823)  
 OTHER INFORMATION: n equals a,t,g, or c  
 US-09-925-300-486

Alignment Scores:  
 Pred. No.: 1,75e-162 Length: 2572  
 Score: 1250.00 Matches: 246  
 Percent Similarity: 99.19% Conservative: 0  
 Best Local Similarity: 99.19% Mismatches: 1  
 Query Match: 98.58% Indels: 1  
 DB: Gaps: 0

US-09-705-500a-3 (1-247) x US-09-925-300-486 (1-2572)

QY 1 MetLeuGlnAsnSerAlaValIleuLeuValIleSerAlaSerAlaThrHisGlu 20  
 Db 265 ATGCTCCAAACCTCAGAGAGCTTCTGGTGTGATCAGCTTCTCAACCCATGAG 324  
 QY 21 AlAGlGlnAsnAspSerValSerProArgLysSerArgValAlaIaGlnAsnSerAla 40  
 Db 325 GCGGAGAGAGATGACTCTGTGAGCCCGAGAAATCCCGAGTGGCGGCTCAAACTAGCT 384  
 QY 41 GluValValArgCysIleuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
 Db 385 GAAGTGTGCTGCTGCTCAACAGTCTCAACAGTGGCGGCTTGTGATGCCG 444  
 QY 61 GlnAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
 Db 445 GAATCTCCACCTCTGACACAGATGGATGTATGACATCTGTAAATCTTCTGTACGC 504  
 QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValIysGlnSerLeuLysCysIleAla 100  
 Db 505 GCTGCTAAATTTGACACTCAGGAGAAAGCATCTGTCAAAAGAGCTTAAATGCATCGCC 564  
 QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
 Db 565 AAGGGGTCCCTCCAGAGTCTTCTGGCATTGGAGGGTCCCATCTTCCAAAGAGATG 624  
 QY 121 IleAlaGlnValGlnGlnGlnCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
 Db 625 ATTGCTGAGGTGAGGAGAGAGTCTACAGCACTGAATGTGTCAGCATCCGCAAGCGC 684  
 QY 141 AsnProGlnAlaIleThrGlnValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
 Db 685 AACCTCGAAACCTCATCTGAGGTGCTCCAGCTGCCAATCACTTCCCAACAGATCTAT 744  
 QY 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp 180  
 Db 745 AACAGACTTCCGAAACCTGCTGGAATGTGATGAAGACACAGCTCAGCAATCAGAGC 804  
 QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAs 200  
 Db 805 AGCTGTGAGAGAAATTNGGGCTTAAACATGCGCACTCTTCCATCCTCGAGACAGA 864  
 QY 200 pHASysValAGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlnProG 220  
 Db 865 CCACTGCGCCCAACACACACACAGAGCTTCAACAGAGACGACCAACATGAGCGCA 924  
 QY 220 nLysLeuLysValIleuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleL 240  
 Db 925 GAAGCTGAAGTCTCTCTCGAAGAACTCCGAGGTGAGAGAGATCTCCTCCACATCAA 984

QY 240 sArgThrSerHisGlnSerAla 247  
 Db 985 ACGCACATCCCATGAGAGTGA 1006

RESULT 13

US-09-778-320-149

Sequence 149, Application US/09778320  
 Patent No. US20010034052A1  
 GENERAL INFORMATION:  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Day, Craig H.  
 APPLICANT: Jiang, Yuguo  
 APPLICANT: Houghton, Raymond L.  
 APPLICANT: Mitcham, Jennifer  
 APPLICANT: Wang, Tongtong  
 APPLICANT: McNeill, Patricia D.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 FILE REFERENCE: 210121.491C5  
 CURRENT FILING DATE: US/09/778,320  
 NUMBER OF SEQ ID NOS: 301  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 149  
 LENGTH: 585  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURES:  
 NAME/KEY: misc feature  
 LOCATION: (1)...(585)  
 OTHER INFORMATION: n=A,T,C or G  
 US-09-778-320-149

Alignment Scores:  
 Pred. No.: 2.01e-109 Length: 585  
 Score: 861.00 Matches: 166  
 Percent Similarity: 98.22% Conservative: 0  
 Best Local Similarity: 98.22% Mismatches: 3  
 Query Match: 67.90% Indels: 0  
 DB: Gaps: 0

US-09-705-500a-3 (1-247) x US-09-778-320-149 (1-585)

QY 79 TyrSerAlaIleAlaLysPheAspThrGlnGlyLysAlaPheValIysGlnSerLeuLysCys 98  
 Db 6 TACANCACTGTAATTTGACACTNANGAAGAAACATTCGTCAAAGAGCTTAAATGC 65  
 QY 99 IleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGln 118  
 Db 66 ATCGCAACGGGGTCACTCCCAAGTCTTCTCCCAATTCGAGGTCTCCACTTCCAA 125  
 QY 119 ArgMetIleAlaGlnValGlnGlnGlnCysTyrSerLysLeuAsnValCysSerIleAla 138  
 Db 126 AGATGATTTGCTGAGGTGAGGAGAGAGTGTACAGCAAGCTGAATGTGTGAGCATGGCC 185  
 QY 139 LysArgAsnProGlnAlaIleThrGlnValAlaGlnLeuProAsnHisPheSerAsnArg 158  
 Db 186 AAGCGAACCCTGGAAGCATCATGAGGTGCTCCAGCTGCCCAATCACTTCCCAACAGA 245  
 QY 159 TyrTyrAsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIle 178  
 Db 246 TACTATAACAACCTTGTCCGAAGCTCTGGAAGTGTGATGAAGACAGATGACCAATTC 305  
 QY 179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198  
 Db 306 AGAGCAACCTCGATGAGAGAAATTTGGGCTTACATGCGCACTCTTCCATCCTCGAG 365  
 QY 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGln 218  
 Db 366 ACAGACCACTGTGCCCAACACACCCACGAGCTCACTTCAACAGAGACGACCAATGAG 425  
 QY 219 ProGlnLysLeuLysValIleuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHis 238

DB 426 CCGCAAGAGCTGAAAGTCTCTCCACAGAACTTCGAGAGGAGAGACTCTCCCTCCAC 485

Qy 239 ILeysArgThrsHsguserAla 247

DB 486 ATCAAAAGCAATCCCATGAGAGTGA 512

## RESULT 14

US-09-910-689-149  
Sequence 149, Application US/09910689  
Patent No. US20020081609A1  
GENERAL INFORMATION:  
APPLICANT: Dillon, Davin C.  
APPLICANT: Day, Craig H.  
APPLICANT: Jiang, Yugu  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Mitcham, Jennifer  
APPLICANT: Wang, Tonglong  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.491C6  
CURRENT APPLICATION NUMBER: US/09/910,689  
CURRENT FILING DATE: 2001-07-20  
NUMBER OF SEQ ID NOS: 307  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 149  
LENGTH: 585  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 10, 30, 32, 527, 565  
OTHER INFORMATION: n = A,T,C or G  
US-09-910-689-149

## Alignment Scores:

Pred. No.: 2,01e-109 Length: 585  
Score: 861.00 Matches: 166  
Percent Similarity: 98.22% Conservative: 0  
Best Local Similarity: 98.22% Mismatches: 3  
Query Match: 67.90% Indels: 0  
DB: 9 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-910-689-149 (1-585)

Qy 79 TyrsSerAlaAlaIysPheAspThrGlnGlyLysAlaPheValIysGlnSerLeuLysCys 98

DB 6 TACANCACTGCTAAATTGACACTNANAGAAAGCAATTCGCAAGAGCTTAAATGC 65

Qy 99 ILeAlaasnGlyValThrsLysValPheLeuAlaIleArgArgCysSerThrPheGln 118

DB 66 ATGCCAAGCGGGTCACTCCCAAGTCTTCTCCGCAATTCGAGGGTCTCCACTTCCAA 125

Qy 119 ArgMetIleAlaGlnGluGlnGluCysTyrsLysLeuAsnValCysSerIleAla 138

DB 126 AGAGTAGTTGCTAGAGTGACGAGAGAGTCTACAGCAAGCTGAATGTGCGAGCATCGCC 185

Qy 139 LysArgAsnProGlnAlaIleThrGlnValIleGlnLeuProAsnHisPheSerAsnArg 158

DB 186 AACCGAACCCTGAAGCCATCACTGAGTCTCCACTGCCAATCACTTCCCAACAGA 245

Qy 159 TyrtTyrsAsnArgLeuValArgSerLeuLeuGluCysAspGlnAspThrValSerThrIle 178

DB 246 TACTATAACAGACTTGTCCGAAAGCTTCGGAATGATGAAGACACATCGACCAAC 305

Qy 179 ArgAspSerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198

DB 306 AGGAGACAGCTGATGAGAAATTTGGCTTACATGCGACCTCTTCCACATCTTCGAG 365

Qy 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlu 218

DB 366 ACAGACCACTGTGCCCCAAACACACCCAGAGTGAATCTTCAACAGAGAGACCAATGAG 425

Qy 219 ProGlnLysLeuLysValIleLeuArgAsnLeuArgGlyGlnGluAspSerProSerHis 238

DB 426 CCGCAGAGCTGAAAGTCTCTCCAGAACTTCGAGAGGAGAGAGACTCTCCCTCCAC 485

Qy 239 ILeysArgThrsHsguserAla 247

DB 486 ATCAAAAGCAATCCCATGAGAGTGA 512

## RESULT 15

US-10-010-742-149  
Sequence 149, Application US/10010742  
Publication No. US20020146727A1  
GENERAL INFORMATION:  
APPLICANT: Dillon, Davin C.  
APPLICANT: Day, Craig H.  
APPLICANT: Jiang, Yugu  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Wang, Tonglong  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Bennington, Angela Ann  
APPLICANT: Zehnener, Barbara  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.491C7  
CURRENT APPLICATION NUMBER: US/10/010,742  
CURRENT FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 307  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 149  
LENGTH: 585  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 10, 30, 32, 527, 565  
OTHER INFORMATION: n = A,T,C or G  
US-10-010-742-149

## Alignment Scores:

Pred. No.: 2,01e-109 Length: 585  
Score: 861.00 Matches: 166  
Percent Similarity: 98.22% Conservative: 0  
Best Local Similarity: 98.22% Mismatches: 3  
Query Match: 67.90% Indels: 0  
DB: 13 Gaps: 0

US-09-705-500A-3 (1-247) x US-10-010-742-149 (1-585)

Qy 79 TyrsSerAlaAlaIysPheAspThrGlnGlyLysAlaPheValIysGlnSerLeuLysCys 98

DB 6 TACANCACTGCTAAATTGACACTNANAGAAAGCAATTCGCAAGAGCTTAAATGC 65

Qy 99 ILeAlaasnGlyValThrsLysValPheLeuAlaIleArgArgCysSerThrPheGln 118

DB 66 ATGCCAAGCGGGTCACTCCCAAGTCTTCTCCGCAATTCGAGGGTCTCCACTTCCAA 125

Qy 119 ArgMetIleAlaGlnGluGlnGluCysTyrsLysLeuAsnValCysSerIleAla 138

DB 126 AGAGTAGTTGCTAGAGTGACGAGAGAGTCTACAGCAAGCTGAATGTGCGAGCATCGCC 185

Qy 139 LysArgAsnProGlnAlaIleThrGlnValIleGlnLeuProAsnHisPheSerAsnArg 158

DB 186 AACCGAACCCTGAAGCCATCACTGAGTCTCCACTGCCAATCACTTCCCAACAGA 245

Qy 159 TyrtTyrsAsnArgLeuValArgSerLeuLeuGluCysAspGlnAspThrValSerThrIle 178

DB 246 TACTATAACAGACTTGTCCGAAAGCTTCGGAATGATGAAGACACATCGACCAATC 305

```

QY 179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
Db 306 AGAGACAGCCTGATGAGAAAATTGGGCTTAACATGGCCAGCCTTCCACATCTGCGAG 365
QY 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGln 218
Db 366 ACAGACCACTGTGCCAAACACACACGAGCTGACTTCAACAGAGACGACCAATGAG 425
QY 219 ProGluLysLeuValLeuLeuArgAsnLeuArgGlyGluAspSerProSerHis 238
Db 426 CCGGAGAGCTGAAGTCTCTCGAGAACTCCGAGGTGAGGAGACTCTCTCCCGAC 485
QY 239 IleLysArgThrSerHisGlnSerAla 247
Db 486 ATCAAACGACATCCCATGAGAGTGCA 512

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Search completed: November 22, 2004, 19:26:25  
 Job time : 540 secs

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QY 21 AlagluGlnAsnSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB 345 GCGAGAGATATACCTCTGTGAGCCCGAGAAATCCCGAGTGGCGCTCAAACTCAGCT 404
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCysLeu 60
DB 405 GAAGTGGTTCGTCCTCCCAACAGTCTTACAGTCCGGCTGGCGGCTTTTGATGCTCG 464
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB 465 GAAACCTCCACCTGTGACACAGATGGATGTATGATCATCTGTAACTCTTTGTACAC 524
QY 81 AlAlaIlePheAspThrGlnGlyLysAlaPheValIleGlySerLeuTyrCysIleAla 100
DB 525 GCTGCTAAATTTACACTCAGGAGAAAGCATTCGTCAAGAGAGCTTAAATGATCCGCC 584
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB 585 AACGGGTGACCTCCACAGGTCTCTCCGCTCCATTCGAGGTGCTCCACTTCCAAAGAGATG 644
QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB 645 ATTGCTAGGTGCGAGAGAGTCTTACAGCAAGCTGATGTGTGACAGCATCCGCAAGCGG 704
QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
DB 705 AACCTGAACCATCACTGAGTGTGCTGCTCCCAATCACTTCCAAACAGATCTAT 764
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
DB 765 AACGACTTGTCCGAACCTGTGTGATGTATGATGAACACATCCACATCCAGAGAC 824
QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB 825 AGCTGTATGAGAAATATGGGCTTAACATGCGCAGCTCTTCCATCTCGACAGACAGAC 884
QY 201 HisCysAlaGlnThrHisProAlaGlnAspPheAsnArgArgThrArgGlnArgGln 220
DB 885 CACTGTGCCCAACACACCCACAGCTGACTTCAACAGAGAGAGACCAATGAGCGCAG 944
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
DB 945 AAGCTGAAGTCTCTCCCAAGAACTCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1004
QY 241 ArgThrSerHisGluSerAla 247
DB 1005 CGCACATCCATCGATGAGTGA 1025

```

## RESULT 2

```

US-10-956-160-4242
; Sequence 4242, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4242
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-4242

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## Alignment Scores:

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Pred. No.: 1,44e-35 Length: 422
Score: 366.00 Matches: 75
Percent Similarity: 98.68% Conservative: 0
Best Local Similarity: 98.68% Mismatches: 0
Query Match: 28.86% Indels: 1

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DB: 6 Gaps: 0
US-09-705-500a-3 (1-247) x US-10-956-160-4242 (1-422)
QY 1 MetLeuGlnAsn-SerAlaValLeuValIleSerAlaSerAlaThrHisG1 20
DB 195 ATGCTCCAAATCTCAGAGAGTCTTGTGCTGTATAGTCTTCTCAACCATGA 254
QY 20 uAlaGluGlnAsnSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAl 40
DB 255 GCGGAGCAGATATTTCTGTGAGCCCGAGAAATCCCGGTGGCAGCTCAGAACTCAGC 314
QY 40 aGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCysLe 60
DB 315 TGAAGTGGTTCGTCCTCCACAGTCTTGCAGGTGGCTGGCGGCTTTTGATGCTCG 374
QY 60 uGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLys 75
DB 375 GGAAGACTCCACCTGTGACACAGATGGATGTATGATCATCTGTAAA 420

```

## RESULT 3

```

US-10-956-160-214349
; Sequence 214349, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214349
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-214349

```

## Alignment Scores:

```

Pred. No.: 1,44e-35 Length: 422
Score: 366.00 Matches: 75
Percent Similarity: 98.68% Conservative: 0
Best Local Similarity: 98.68% Mismatches: 0
Query Match: 28.86% Indels: 1
DB: 6 Gaps: 0

```

US-09-705-500a-3 (1-247) x US-10-956-160-214349 (1-422)

```

QY 1 MetLeuGlnAsn-SerAlaValLeuValIleSerAlaSerAlaThrHisG1 20
DB 195 ATGCTCCAAATCTCAGAGAGTCTTGTGCTGTATAGTCTTCTCAACCATGA 254
QY 20 uAlaGluGlnAsnSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAl 40
DB 255 GCGGAGCAGATATTTCTGTGAGCCCGAGAAATCCCGGTGGCAGCTCAGAACTCAGC 314
QY 40 aGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCysLe 60
DB 315 TGAAGTGGTTCGTCCTCCACAGTCTTGCAGGTGGCTGGCGGCTTTTGATGCTCG 374
QY 60 uGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLys 75
DB 375 GGAAGACTCCACCTGTGACACAGATGGATGTATGATCATCTGTAAA 420

```

## RESULT 4

```

US-10-900-423-12
; Sequence 12, Application US/10900423
; GENERAL INFORMATION:
; APPLICANT: GOTO, MASAAKI
; APPLICANT: TOMOYASU, AKIHIRO
; APPLICANT: YANO, KAZUKI
; APPLICANT: KOBAYASHI, FUMIE

```

```

APPLICANT: NAKAGAWA, NOBUAKI
APPLICANT: YASUDA, HISATAKA
APPLICANT: YAMAGUCHI, KYOJI
APPLICANT: KINOSAKI, MASAHITO
APPLICANT: MOCHIZUKI, SHIN-ICHI
APPLICANT: NAKAKARUWAI, TADASHI
APPLICANT: MORINAGA, TOMONORI
APPLICANT: TSUDA, SISUKE
APPLICANT: HIGASHIO, KANUJI
TITLE OF INVENTION: NOVEL PROTEIN AND PROCESSES FOR PRODUCING THE SAME
FILE REFERENCE: 239674USOPCT
CURRENT APPLICATION NUMBER: US/10/900,423
PRIOR FILING DATE: 2004-07-28
PRIOR APPLICATION NUMBER: US/09/647,907
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/JP99/01906
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: JP 243355/1998
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: JP 99741/1998
PRIOR FILING DATE: 1998-04-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 862
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-900-423-12

```

```

Alignment Scores:
Pred. No.: 1,236-33      Length: 862
Score: 354.00           Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92%      Indels: 12
DB: 6                  Gaps: 4

```

US-09-705-500a-3 (1-247) x US-10-900-423-12 (1-862)

```

Qy 9 LeuValIleuValIleSer-----AlaSerAlaThrHisGluAla 21
Db 7 CTGGCTTGTGTGTGGCCACCTTGACCGCGCGGGAGCGACGACCGACCAACCCACC 66
Qy 22 Glu--GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 67 GAGGGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 127 GAGATTCAGACCTGTGTGTCACAGCTGGCGATGAGTGGGAGTGGGCTGTGTGATGATTTTC 186
Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 187 GAGAACCACTCTGTGATTCGGGGCTTACATGAGTTTGATTCATCTTTTCGCAACAC 246
Qy 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysTleAla 100
Db 247 GCTGGAAATTTATATGCGCCAGGCAAGTCACTTCATAAAGACCCCTTGAAATGTAAAGGC 306
Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 307 CACGCTCTGGGCAACAGCTTCGGCTCGCATTAAGCCGAAGTCCCGGCCCATCAGGAAATG 366
Qy 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 367 GTGTCCAGATGGCAGCGGAGATCTACCTCAACAGACAGACTGTGCGCGCTCCCGCAGAG 426
Qy 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 427 AACACCCGGGTGATAGTGGAGATGATCCATTTCAGAGACTTGTGTGTGACGAACCTTTC 486
Qy 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp 180

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Db 487 GTGACCTCTGTGAACCTTGCTGTGACCTGTGGGGAAGAGTGAAGAGCCATCACCAC 546
Qy 161 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 547 AGCGTGCAGGTTCAGTGTGACAGAGACTGGGGAAGCCCTGTCTCCATCTTG-----AGC 600
Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgA-GArgThrAsnGluProGln 220
Db 601 TTCTGCACCTGGGC-CATCCAGAAAGCTCCCAAGCGCGCCCGCCAGCCCAAGCCAGGT 659
Qy 221 LysLeuLysValIleLeuArgAsn--LeuArgGlyGluGluAspSerPro 236
Db 660 GAGACAGAACCAAGCTCTCCAGGGCCACACAGGGGGAAGACAGACATCACT 710

```

# RESULT 5

```

US-10-956-157-1106
Sequence 1106, Application US/10956157
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
FILE REFERENCE: 031896-043000 (AW 101081)
CURRENT FILING DATE: US/10/956,157
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1106
LENGTH: 2380
TYPE: DNA
ORGANISM: Homo sapiens
US-10-956-157-1106

```

```

Alignment Scores:
Pred. No.: 5,286-33      Length: 2380
Score: 354.00           Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92%      Indels: 12
DB: 6                  Gaps: 4

```

US-09-705-500a-3 (1-247) x US-10-956-157-1106 (1-2380)

```

Qy 9 LeuValIleuValIleSer-----AlaSerAlaThrHisGluAla 21
Db 168 CTGGCTTGTGTGTGGCCACCTTGACCGCGCGGGAGAGCGACCGACCAACCCACC 227
Qy 22 Glu--GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 228 GAGGGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 287
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 288 GAGATTCAGACCTGTGTGTCACAGCTGGCGATGAGTGGGAGTGGGCTGTGTGATGATTTTC 347
Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 348 GAGAACCACTCTGTGATTCGGGGCTTACATGAGTTTGATTCATCTTTTCGCAACAC 407
Qy 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysTleAla 100
Db 408 GCTGGAAATTTATATGCGCCAGGCAAGTCACTTCATAAAGACCCCTTGAAATGTAAAGGC 467
Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 468 CACGCTCTGGGCAACAGCTTCGGCTCGCATTAAGCCGAAGTCCCGGCCCATCAGGAAATG 527
Qy 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 528 GTGTCCAGATGGCAGCGGAGATCTACCTCAACAGACAGACTGTGCGCGCTCCCGCAGAG 587
Qy 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160

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Db 588 AACACCCGGGTGATGATGATGATCATTCATCAAGACCTTGCTGTCAGCAGAACCTTAC 647
Qy 161 AAsArLeuValArgeSerleuLeuGluCyAspGluAspThrValSerThrIleArgAsp 180
Db 648 GTGACCTGTGTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 707
Qy 181 SerLeuMetGluLysIleGlyProAspMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 708 AGGTCAGAGGTGTAGTGTAGCAGAACTGGGGAAGCTGTGCTCCACTTGTG-----AGC 761
Qy 201 HisCyAlaGlnThrIleSPROArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
Db 762 TTCTGACCTCGGC-CATCCAGAAAGCTCCACCGCGCCCCCGAGCGCCAGCCCGAGGT 820
Qy 221 LysLeuLysValLeuLeuArgAsn--LeuArgGlyGluGluAspSerPro 236
Db 821 GGAACAAGAACCAAGCTCTCCAGGCGCCACACCGGGAAGAGAGATCACT 871

RESULT 6
US-60-615-573-13086
/ Sequence 13086, Application US/60615573
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William M
/ APPLICANT: Murphy, Ellen
/ APPLICANT: Olmsted, Stephen
/ TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
/ FILE REFERENCE: 031896-084099 (AM 101724)
/ CURRENT APPLICATION NUMBER: US/60/615,573
/ CURRENT FILING DATE: 2004-10-05
/ NUMBER OF SEQ ID NOS: 18598
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 13086
/ LENGTH: 2025
/ TYPE: DNA
/ ORGANISM: Staphylococcus epidermidis
US-60-615-573-13086

Alignment Scores:
Pred. No.: 0.24 Length: 2025
Score: 93.50 Matches: 47
Percent Similarity: 40.28% Conservative: 38
Best Local Similarity: 22.27% Mismatches: 86
Query Match: 7.37% Indels: 40
Gaps: 9
DB: 8

US-09-705-500a-3 (1-247) x US-60-615-573-13086 (1-2025)
Qy 14 SerAlaSerAlaThrHisGluAlaGluGlnAsnAspSer-ValSerProArgLysSerAr 33
Db 746 AGTATCAACAGTAACTCAACGATTGAACAAATCAAGCTATTCACCAAAATTAACAGA 805
Qy 33 gValAlaA-----AlaGlnAsnSerAlaGluValAlaValArgCysLeuAsnSe 48
Db 806 AGCTATCAACAGTCTTCMAAACCAAGAAATAATATACGAATTGTAATGCTMAAAACAG 865
Qy 48 rAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThrCysAspThrAs 68
Db 866 A-----CTTGAATAAGCAGTAAATGATACAGA 892
Qy 68 pGlyMetTyrAspIleCysLysSerPheLeu-----TyrSerAlaAlaLysPheAspTh 86
Db 893 TCACAACACAGCGTATGCTCAAGAAACAATTAAATTAATTCACAGCTTMAAAAGGAGAAC 952
Qy 86 rGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGly-----102
Db 953 TCMAAATGAA-----ATACAAAAGGCAACATGATTTATTAATGAAGATGCTACTGC 1006
Qy 103 -----ValThrSerLysValPheLeuAlaIleArgArgCys 114
Db 1007 TCAAGATATTTCTTCTGAAAAATCTAAAGTAGAGCAAGATTAACAAGCATTTCAAAATGC 1066
Qy 114 sSerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeu-----132
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```
Db 1067 TAAAGATGACTTAAGACCTGATTAAGAGAAATTACAGACTGCATCAATTAACCTTATACA 1126
Qy 133 -AsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuPr 152
Db 1127 AAATGTTAATACCAATGTAAATAA-----CCATCTAGATTCAAAACATTAAGTCTGCAAG 1183
Qy 152 AsnHisPheSerAsnArgTyr-----TyrAsnA-GluValAlaArgSerLeuLeuGly 170
Db 1184 ACGAAATATCGAAACCAAAATATATATACCGCTTAAAAAATGAAGACATATGTTCTGAAAA 1243
Qy 170 sAspGluAspThrValSerThrIleArgAspSerLeu-----MetGluLysIleGlyPr 188
Db 1244 TACAAACCTTACTTATTAATGACAGTAAAGATGCTTTAAGCTAATGAATTAATGCAATTCAC 1303
Qy 188 AsnMetAlaSerLeuPheHisIleLeuGln 198
Db 1304 AGAGTTTACAAAAGCTATTAATATACTTCAA 1334

RESULT 7
US-60-620-788-64
/ Sequence 64, Application US/60620788
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Sellman, Bret R.
/ APPLICANT: Baker, Steve M.
/ TITLE OF INVENTION: Immunogenic Compositions of Staphylococcus epidermidis Antigens
/ FILE REFERENCE: AM101548 L
/ CURRENT APPLICATION NUMBER: US/60/620,788
/ CURRENT FILING DATE: 2004-10-21
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 64
/ LENGTH: 30612
/ TYPE: DNA
/ ORGANISM: Staphylococcus epidermidis
US-60-620-788-64

Alignment Scores:
Pred. No.: 12.8 Length: 30612
Score: 93.50 Matches: 47
Percent Similarity: 40.28% Conservative: 38
Best Local Similarity: 22.27% Mismatches: 86
Query Match: 7.37% Indels: 40
Gaps: 9
DB: 8

US-09-705-500a-3 (1-247) x US-60-620-788-64 (1-30612)
Qy 14 SerAlaSerAlaThrHisGluAlaGluGlnAsnAspSer-ValSerProArgLysSerAr 33
Db 8904 AGTATCAACAGTAACTCAACGATTGAACAAATCAAGCTATTCACCAAAATTAACAGA 8963
Qy 33 gValAlaA-----AlaGlnAsnSerAlaGluValAlaValArgCysLeuAsnSe 48
Db 8964 AGCTATCAACAGTCTTCMAAACCAAGAAATAATATACGAATTGTAATGCTMAAAACAG 9023
Qy 48 rAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThrCysAspThrAs 68
Db 9024 A-----CTTGAATAAGCAGTAAATGATACAGA 9050
Qy 68 pGlyMetTyrAspIleCysLysSerPheLeu-----TyrSerAlaAlaLysPheAspTh 86
Db 9051 TCACAACACAGCGTATGCTCAAGAAACAATTAAATTAATTAACAGCTTMAAAAGGAGAAC 9110
Qy 86 rGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGly-----102
Db 9111 TCMAAATGAA-----ATACAAAAGGCAACATGATTTAATTAATGAAGATGCTACTGC 9164
Qy 103 -----ValThrSerLysValPheLeuAlaIleArgArgCys 114
Db 9165 TCAAGATATTTCTTCTGAAAAATCTAAAGTAGAGCAAGATTAACAAGCATTTCAAAATGC 9224
Qy 114 sSerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeu-----132
```



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Db 9225 TAAAGATGACTTAAGACGTGATTAAGAGATTACACATCGCATACATTAACCTTTATCA 9284
QY 133 -AsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuPr 152
Db 9285 AAATGTTAATACCATGCTAAATAA---CCATCTAGATTCAAAACATTAAGTCTGCAAG 9341
QY 152 AsnHisPheSerAspArgTyr-----TyrAsnArgLeuValArgSerLeuGluGly 170
Db 9342 ACCAAATATGCAAAACCAATATTAATACCGCTAAATAATGAACCATTAATGTTCTGAAA 9401
QY 170 AspGluAspThrValSerThrIleArgAspSerLeu-----MetGluLysIleGlyPr 188
Db 9402 TACAAACCTCACTGTTAAATGACAGTAAAGATGCTTTACGTAAAGATTAATCAATTCAC 9461
QY 188 AsnMetAlaSerLeuPheHisIleLeuGln 198
Db 9462 AGAGTTTACAAAAGCTATTAATATCTTCAA 9492

```

# RESULT 8 US-10-968-812-1

```

; Sequence 1, Application US/109688012
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; APPLICANT: Curtis, Roy A. J.
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL HUMAN GENES AND METHODS OF USE THEREOF
; FILE REFERENCE: 10448-195001
; CURRENT APPLICATION NUMBER: US/10/968, 812
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/10/176, 306
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/001, 137
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/45291
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/248, 362
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/248, 331
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/248, 365
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/250, 077
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250, 327
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250, 176
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 10/023, 617
; PRIOR FILING DATE: 2001-12-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3134
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)...(2131)
; US-10-968-812-1

```

## Alignment Scores:

```

Pred. No.: 3.25 Length: 3134
Score: 86.50 Matches: 55
Percent Similarity: 37.02% Conservative: 42
Best Local Similarity: 20.99% Mismatches: 102
Query Match: 6.82% Indels: 63
DB: 6 Gaps: 13

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US-09-705-500A-3 (1-247) X US-10-968-812-1 (1-3134)

```

QY 15 AlaSerAlaThrHisGluAlaGluGlnAsnAspSerValSerProAlaGlySer----- 32
Db 89 GCGTCTCAACCCACGCGGAGAGCATGACAGAAAAGACATTAAGAGAGTCCACCGAG 148
QY 33 -----ArgValAlaAlaGlnAsnSerAlaGluValAlaArg----- 44
Db 149 GAATGACACCGGAAAATAGAGAGGCGAGCGCGCCCGCCCAAGTGGCGGCGACAGACA 208
QY 45 Cys-----LeuAsnSerAlaLeuGlnValGlyCysGlyAla 56
Db 209 TGCCCCACCCCTCGGGAATACAGCAAGTCACTGCTTCCATGAACCTGGCG----- 259
QY 57 PheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSer 76
Db 260 -----CTGCTAGAGTGAAGGGCGGCTGCGACGAAGTGAAGTCTGAGAAATGC----- 307
QY 77 PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96
Db 308 -----ATCCAGTCTCTCGATTCACTGCGACGCTGCGACAGAGACACATG 355
QY 97 LysCysIleAlaAsnGlyValThrSerLysValPhe-----LeuAlaIleArg 112
Db 356 CTCAACATGCTGCTGCGCATGACAGCTGGGAGTGGCCGCTCCGCCGACCTGGCTGCCGC 415
QY 113 ArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlyCysTyrSerLysLeu 132
Db 416 CTGCTGACCTCATACACAGAGCCACAGGGGACACCCAGAG-----CTGAGACGGCTG 469
QY 133 AsnValCysSerIleAlaLys-----ArgAsnProGluAlaIleThrGluVal 148
Db 470 CAGATCTCACTGCTGACGATGACTGCTGATGCGACACCTGAGGTGATGACCCAGAT 529
QY 149 ValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeu 168
Db 530 CCCCAGCTA---GAAGAAGTCAATAGTGTCTTCTGGGCGACCGTGGCCGGAG----- 580
QY 169 GluCysAspGluAspThrValSerThrIleArgAspSer-----LeuMetGluLysIle 186
Db 581 -----GGCAACTCAGCCCGACAGAAAGACTGGAGACTTCTGACCTTCGAGCCCTGGT 634
QY 187 GlyPro-----AsnMetAla 191
Db 635 GGCCTTGCGCCCCCACTCCCAATGACAGCCAGCCGCGGCAAAAGCGCAAGTGTCC 694
QY 192 SerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPhe 211
Db 695 TTGCTTTTCGACCACTTGAGACGGGAGGAGTGGCTGACACCTCACTGAGAGTTC 754
QY 212 AsnArgArgArgThrAsnGluProGlnLysLeuLys-----ValLeuLeuArgAsnLeu 229
Db 755 CGGTCTTCCAGGCTATGACCCCGAGGACTGGGAGCTGAGCTGTTTTCAGAGGCTCAGTA 814
QY 230 ArgGly 231
Db 815 CGAGGC 820

```

## RESULT 9

```

; US-60-615-573-12667
; Sequence 12667, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeeth
; APPLICANT: Mounts, William M.
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615, 573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12667
; LENGTH: 1965

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; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-60-615-573-12667

Alignment Scores:
Pred. No.: 2.17 Length: 1965
Score: 85.50 Matches: 42
Percent Similarity: 38.41% Conservative: 21
Best Local Similarity: 25.61% Mismatches: 70
Query Match: 6.74% Indels: 31
DB: 8 Gaps: 6

US-09-705-500a-3 (1-247) x US-60-615-573-12667 (1-1965)

QY 35 AlaAlaGlnSerSerIaIaIaValArgCysLeuAsnSerAlaLeuGlnValGlyCys 54
Db 67 AGTCGGAAGAACTTGCTACTGAAATTTAATTACTTGAAGTCAATCTTAAGATTACCTAA 126
QY 55 G1yAlaPheAlaCysLeuGlnAsnSerThrCysAspThrAspGlyMetTyr----- 71
Db 127 GGGACT-----GAAACATTTTGTAGTGAACCTTCATGGTGAATACGAATCTTTC 174
QY 72 -----AspIleCysIys 75
Db 175 CAACATGTTTAAAGAAACGATCGAATGCGCTAATAATTATATATCTTCAAA 234
QY 76 SerPheLeuTyrSerAlaIaIaLysPheAspThrGlnGlyLysAlaPheVal---LysGln 94
Db 235 GATTAATTAATCCAGCAAGAAATCAACGACTTAGCAACATTTAGTATACATCCGGAAGA 294
QY 95 SerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCys 114
Db 295 AAACATAAATTAAGTAAATAATTAATTCGATTCATCGAACAATTAAATTTGGTATATT 354
QY 115 SerThrPheGlnArgMetIleAlaGlnValGlnGluCysTyrSerLysLeuAsnVal 134
Db 355 ACAACATTCAAGCATTAAT---GATTTAATACATATTGCTCCACAAATATACACT 411
QY 135 CysSerIleAlaLysArgAsnProGln-----AlaIleThrGlnValValGln 150
Db 412 TCAAAATTCGCAACCATTAACCTGAACATACGTTATATATTATGAAGCTACTTAC 471
QY 151 LeuProAsnHisPheSerAsnArg-----TyrTyrAsnArgLeuValArgSerLeu 168
Db 472 AAGAGCAATGAATTTCTAATTAATAAAGCCTTATATGAACATTAATGTAACCAATTTAT 531
QY 169 GluCysAspGln 172
Db 532 GAATTGAACAA 543

RESULT 10
US-10-746-294A-95/c
; Sequence 95, Application US/10746294A
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Roundley, Steven D.
; APPLICANT: Wiesend, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)E
; CURRENT APPLICATION NUMBER: US/10/746, 294A
; PRIOR FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 09/692,412
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 09/803,736
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 124
; SEQ ID NO 95
; LENGTH: 129516
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-746-294A-95

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Alignment Scores:
Pred. No.: 1.15e+03 Length: 129516
Score: 85.00 Matches: 48
Percent Similarity: 39.30% Conservative: 31
Best Local Similarity: 23.88% Mismatches: 57
Query Match: 6.70% Indels: 65
DB: 6 Gaps: 11

US-09-705-500a-3 (1-247) x US-10-746-294A-95 (1-129516)

QY 62 AsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAla 81
Db 44853 AACAGCACT-----AACATCAACCAAGCTGACCTCCATGTTCCAG 44815
QY 82 AlaLysPheAspThrGlnGlyLysAlaPheValLysLeuSerLeuLys----- 97
Db 44814 CCAATCTTCAACAGGTAGCTGCTTCTTCTGAGCTCCGCTTCGACTCTTGTAGTA 44755
QY 98 CysIle-----AlaAsnGlyValThrSerLysValPheLeuAlaIle--- 111
Db 44754 TGTGTGGCTCTATCAAAACTGCTCGCATGTTCATATGATCTTCTTGGCTTGAGC 44695
QY 112 -----ArgArgCysSerThrPheGlnArg-----MetIleAlaGlnValGln 125
Db 44694 AGCAGAACTTCAAACTTTGCCAAACTAAGCCACACACTTGTAAATGCTTTAGCGTCCA 44635
QY 126 Glu-----GluCys-----TyrSerLysLeuAsn 133
Db 44634 GAGTCGCTCATATAAGCTCGTGTCTCTTAATTCCTAGTATATCTCAAGTCAAT 44575
QY 134 ValCysSerIleAlaLysArgAsnProGlnAlaIleThrGlnValValGln---LeuProAs 153
Db 44574 GTATGCCCATTAAGAGAGTCCGGGGGTCAAGAAACAGGCTAGATATTGCAAGCTCAAAA 44515
QY 153 HisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuGluCysAspGlnAs 173
Db 44514 TAGCTTAGCTCGTTCGTTCTTCAAGCAAG----- 44487
QY 173 PThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerIle 193
Db 44486 -----AGACCTCTCAAACTCAACCAAACTGGTGCACAGCTACCAACTCT 44443
QY 193 u-----PheHisIleLeuGlnThrAspHisCysAlaGlnThrHis---ProArgAl 209
Db 44442 CAGAGACCATTTCAAGTATACCGGCATACAGCTTTCTCACTATCTATCTTCCCAAGT 44383
QY 209 AspPheAsnArgArgArgThrAsnGluProGlnLysLeuValLeuLeuArgAsnLe 229
Db 44382 GGAGTTCAT-----CTCAATGTATTTCTTGAATAATCT 44350
QY 229 u 229
Db 44349 T 44349

RESULT 11
US-60-613-292-289
; Sequence 289, Application US/60613292
; GENERAL INFORMATION:
; APPLICANT: Gene Logic, Inc
; APPLICANT: Higgs, Brandon
; APPLICANT: ELASHOFF, Michael
; APPLICANT: MENDRICK, Donna L.
; APPLICANT: PORTER, Mark W.
; APPLICANT: CASTLE, Arthur L.
; APPLICANT: JOHNSON, Kory R.
; TITLE OF INVENTION: MOLECULAR TOXICITY MODELS FROM ISOLATED HEPATOCYTES
; FILE REFERENCE: 044921-5135-PR
; CURRENT APPLICATION NUMBER: US/60/613, 292
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 1300
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 289

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; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13040
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-60-615-573-13040

Alignment Scores:
Pred. No.: 2.12 Length: 1197
Score: 83.00 Matches: 44
Percent Similarity: 38.97% Conservative: 32
Best Local Similarity: 22.56% Mismatches: 57
Query Match: 6.55% Indels: 62
DB: Gaps: 11

US-09-705-500a-3 (1-247) x US-60-615-573-13040 (1-1197)

QY 57 PhalaCysLeuGluAsnSerThrCysAspThrAsp-----GlyMetTyr 71
DB 739 TTTATTAAATTTGAAAGAGCTACAACTGATCATCATCTTAACAGAGACTTTAT 798
QY 72 AspIleCysLeuSerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPhe 91
DB 799 GAGCTTATTCATCTTT-----AAAGTAAAGTAAAGAACTGAAAGGAATCATTT 849
QY 92 ValIleGluSerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIle 111
DB 850 TATAGATTGAACGTACGC-----ATTAAATGAGAAACATTTATTTGACACA 894
QY 112 ArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluCysTyrSerLys 131
DB 895 CAAGATTTAATTAATTAATAAGAAATGATTAAGTCTGAGTGAAGAAAAC----- 942
QY 132 LeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValAlaGlnLeu 151
DB 942 ----- 942
QY 152 ProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAsp 171
DB 943 GAAATCAATTTTGT-----TTTATGAAAGATTTAATCTTCATATATGTCAAAATGAC 996
QY 172 GluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMet--- 190
DB 997 GAATGCCATA-----GTTAAAGAGTTTCACACAGATTACTT 1035
QY 191 -----AlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArg 208
DB 1036 GATGATGCCGTCACTTTTGTATTCGGCAATGACTGAT-----TTATATCTTATATCCAAAG 1089
QY 209 Ala-----AspPheAspArg-----ArgArgThrAsnGluPro 219
DB 1090 GCTTTCAAGTTTATTAAGTACATATATGAAATTTGATAAAGTGAGTATGATCATATGCA 1149
QY 220 GlnLysLeuLysValLeuLeuArgAsnLeuArgIleGluGluAsp 234
DB 1150 GAAAGACTT-----TTAAAGATGAATGAGAGGTGAACAAAAT 1188

RESULT 14
US-60-615-573-11206
; Sequence 11206, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573

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; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11206
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-60-615-573-11206

Alignment Scores:
Pred. No.: 1.16 Length: 720
Score: 82.50 Matches: 49
Percent Similarity: 37.25% Conservative: 43
Best Local Similarity: 19.84% Mismatches: 92
Query Match: 6.51% Indels: 63
DB: Gaps: 12

US-09-705-500a-3 (1-247) x US-60-615-573-11206 (1-720)

QY 5 SerAlaValLeuLeuValLeu-----ValIleSerAlaSerAlaThr----- 18
DB 79 AGTCATTTACATTGGACCTCTATTATTTAACGTAAGTAACTGTGTATGGCATGAA 138
QY 19 HisGluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsn 38
DB 139 AATACTCCAAACCAAAATCAAGAACATCACAAAATTCACAGACAGCAGCCTACAAAT 198
QY 39 SerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAla 58
DB 199 AATACTGAA-----AATCAAGATGCCACAGCATTAACA 221
QY 59 CysLeuGluAsnSerThrCysAspThr-----AspGlyMetTyrAspIleCysLysSer 76
DB 232 ACAGATCAAAATTAATATGATGAAAGAAATACGATCGCATATGACTT-----CCA 285
QY 77 PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96
DB 286 ATTCTTATGTAAGTCTGCTGAGCTAGATGATCAAGAAAT--ATTATTAAGATGCTGTG 342
QY 97 Lys----- 97
DB 343 GAAGATGCTAAACCCCTGCTCAGAAAGCAACCGGTGAATTCCTGGGTACCAACAT 402
QY 98 -----CysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCys 114
DB 403 TATGAACTTCTGTGAGTGAACGGAATTAAGTTATTTAT-----CGTAAATTT 453
QY 115 SerThrPheGlnArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnVal 134
DB 454 AGCATGCAACATACCTATATGTTGAAATTAATCAACAGATATATATACAAATTAAGTT 513
QY 135 CysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHis 154
DB 514 GTTGAAACCAACCAATCAAAATTAAGATGAATGAAAGAAAGAAACA-----AATCAA 567
QY 155 PheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThr 174
DB 568 GCATTAATCTTCAGTAACAAATTAACAAATTT--ACCAAAAACGAAAGACGAAACAC 624
QY 175 ValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPhe 194
DB 625 ---AAAACACTAAAGAAAGATTAAGAGAGAAAGAAATCTTAAGACAAATAAACA----- 675
QY 195 HisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArg 214
DB 676 -----CATAAGAAAGCAAAAGAAAGAA 699

RESULT 15
US-60-622-712-2559

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Tue Nov 23 09:18:30 2004

us-09-705-500a-3.rnpu

Page 9

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/ Sequence 2559, Application US/60622712
/ GENERAL INFORMATION:
/ APPLICANT: Klaenhammer, Todd
/ APPLICANT: Russell, William
/ APPLICANT: Alterman, Eric
/ TITLE OF INVENTION: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACIDS AND USES THEREOF
/ FILE REFERENCE: 5051-604PR10
/ CURRENT APPLICATION NUMBER: US/60/622,712
/ CURRENT FILING DATE: 2004-10-27
/ NUMBER OF SEQ ID NOS: 2559
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2559
/ LENGTH: 1993570
/ TYPE: DNA
/ ORGANISM: Lactobacillus acidophilus
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (61484)..(61484)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (62139)..(62139)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (416372)..(416372)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1630403)..(1630403)
/ OTHER INFORMATION: n is a, c, g, or t
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/ NAME/KEY: misc feature
/ LOCATION: (1631417)..(1631417)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1631599)..(1631599)
/ OTHER INFORMATION: n is a, c, g, or t
US-60-622-712-2559
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Pred. No.: 1.23e+05 Length: 1993570
Score: 82.50 Matches: 49
Percent Similarity: 40.31% Conservative: 30
Best Local Similarity: 25.00% Mismatches: 76
Query Match: 6.51% Indels: 42
DB: 8 Gaps: 12
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US-09-705-500a-3 (1-247) x US-60-622-712-2559 (1-1993570)

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QY 66 AspThrAspGlyMetTyraAspIleCysLysSerPheLeuTySerAlaAlaLysPheAsp 85
Db 320540 GATACCTCTTTATACCGCATATTGC-----GTTAAGTTTGAAT 320578
QY 86 ThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaGlnGlyValThrSer 105
Db 320579 ACAATG-----TTTATTATGAAAAAGG-AGGGTT-----AATATGCGCAACA 320619
QY 106 LysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGln 125
Db 320620 GAAGTTTATTTA---GTTCTGTCATGCTGAACGATGTTCAACCAATTGAATTAAGTTCAA 320676
QY 126 GluGluCysTySerLysLeuAsnValCysSerIle-----AlaLysArgAsnProGlu 143
Db 320677 GGTGGAGCGATCTCTCATTAACAGGATTAAAGGATTATGATTAAAAAGAACTGCTAAAT 320736
QY 144 AlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgGlyTyraAsnArgLeu 163
Db 320737 GCTTTAAGTCAAGTA-----CAGTTGATATATGATTCGTCAGACCTTA 320781
QY 164 ValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp---SerLeu 182
Db 320782 AAAAGAGCGAT-----GATACCTGTCATTATGAAAAAGATGCTAATGTG 320825
QY 183 MetGluLysIleGly-----ProAsnMetAlaSerLeuPheHis---Ile 196
Db 320827 GTTTCGATATTGGGAAATTAAGAAAGTGGCAGAAATTCGTGAAGTTTCTTTGGAAGT 320886
QY 197 LeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThr 216
Db 320887 TTCAGGGGTGATGATATTAAACCAACTGGAGTCAAGTGCATGCGAATCGGG 320946
QY 217 AsnGluProGlnLysLeuLysValLeu-----LeuArgAsnLeu 229
Db 320947 CATGAAGATGATGTGGCCAAATTTATTAATAGGTGGATTAGCAAAATTCGTAAGACA 321006
QY 230 ArgGlyGluGluAspSerProSerHisTleLysArgThrSerHisGlu 245
Db 321007 ACTAAGAGCGAGAT---CCACGTCATTATGACAGAAAAATCTCAAGAA 321051
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Search completed: November 22, 2004, 19:27:46  
Job time : 696 secs

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GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: November 22, 2004, 17:49:27 ; Search time 27 Seconds

(without alignments)  
606.687 Million cell updates/sec

Title: US-09-705-500A-3

Sequence: 1 MCONSALLVLTISASATHE.....NLKGEEDSPSHIKRTSHEGA 247

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	247	2	US-08-208-005C-2
2	1268	100.0	247	2	US-09-038-597A-2
3	1268	100.0	247	2	US-08-460-529B-10
4	1268	100.0	247	2	US-08-431-117A-2
5	1268	100.0	247	4	US-09-361-736B-10
6	660.5	52.1	204	2	US-08-208-005C-5
7	660.5	52.1	204	2	US-09-038-597A-5
8	628	49.5	170	2	US-08-460-529B-9
9	628	49.5	170	4	US-09-361-736B-9
10	354.5	28.0	296	3	US-08-831-132-14
11	354.5	28.0	296	3	US-09-416-150-14
12	354	27.9	302	3	US-08-831-132-2
13	354	27.9	302	3	US-09-416-150-2
14	354	27.9	302	4	US-09-193-881-23
15	354	27.9	302	4	US-09-361-736B-12
16	351.5	27.7	251	4	US-09-361-736B-2
17	333.5	26.3	251	2	US-08-460-529B-2
18	91	7.2	901	4	US-09-828-062-8
19	89.5	7.1	10182	3	US-09-134-001C-1159
20	86	6.8	500	4	US-09-198-452A-289
21	85.5	6.7	311	4	US-09-710-279-2460
22	85.5	6.7	656	3	US-09-134-001C-4322
23	83.5	6.6	290	4	US-09-655-908-6
24	83.5	6.6	290	4	US-09-655-908-8
25	83.5	6.6	1027	4	US-09-762-724-8
26	83.5	6.6	1029	4	US-09-762-724-6
27	83	6.5	319	4	US-09-710-279-792

28	83	6.5	319	4	US-09-710-279-2008	Sequence 2008, Ap
29	83	6.5	398	4	US-09-710-279-44	Sequence 44, Appl
30	83	6.5	417	4	US-09-710-279-1498	Sequence 1498, Ap
31	83	6.5	417	3	US-09-134-001C-3810	Sequence 3810, Ap
32	82	6.5	362	3	US-09-134-001C-4670	Sequence 4670, Ap
33	81	6.4	680	3	US-09-298-924-4	Sequence 4, Appl
34	81	6.4	720	2	US-08-840-236-1	Sequence 1, Appl
35	81	6.4	720	2	US-08-505-448A-1	Sequence 1, Appl
36	79.5	6.3	609	4	US-09-538-092-711	Sequence 711, App
37	79.5	6.3	708	1	US-08-145-681-4	Sequence 4, Appl
38	79.5	6.3	708	2	US-08-453-703-4	Sequence 4, Appl
39	79.5	6.3	708	2	US-08-456-106-4	Sequence 4, Appl
40	79.5	6.3	708	3	US-08-456-108-4	Sequence 4, Appl
41	79.5	6.3	708	3	US-09-265-577-4	Sequence 4, Appl
42	79.5	6.3	708	4	US-09-633-739-4	Sequence 4, Appl
43	79	6.2	264	4	US-09-134-000C-5831	Sequence 5831, Ap
44	78.5	6.2	1288	4	US-09-546-934-4	Sequence 4, Appl
45	78	6.2	315	3	US-09-184-964-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-08-208-005C-2  
Sequence 2, Application US/08208005C  
Patent No. 5837498  
GENERAL INFORMATION:  
APPLICANT: OLSEN, ET AL.  
TITLE OF INVENTION: Copolymers of Stannius Protein, Stannocalcin  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/208,005C  
FILING DATE: 8 MARCH 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D,  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 335800-78  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO. 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-208-005C-2  
Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MLQNSAVLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
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Db 61 ENSTCTDGMWDICKSFLYSAAKFDIOGKAFVKSILKCIANGVTSKVFLAIRCSTFORM 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEAITVEVOLPHNFSNRYNRLVRSLLCEDDTVSTIRD 180  
Db 121 IAEVQECYSKLVNCSIAKRNPEAITVEVOLPHNFSNRYNRLVRSLLCEDDTVSTIRD 180  
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Db 181 SLMEKIGPMNASLPHILQTDHCQOTHPRADFNRRRTNEPOKLVLLRNLRGEEDESPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 2  
US-09-038-597A-2  
; Sequence 2, Application US/09038597A  
; Patent No. 5877290  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Corpules of Stannius Protein,  
; TITLE OF INVENTION: Stannicalcin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,597A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,005  
; FILING DATE: 8-MARCH-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-78  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-09-038-597A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLQNSAVLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
Db 1 MLQNSAVLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
QY 61 ENSTCTDGMWDICKSFLYSAAKFDIOGKAFVKSILKCIANGVTSKVFLAIRCSTFORM 120

Db 61 ENSTCTDGMWDICKSFLYSAAKFDIOGKAFVKSILKCIANGVTSKVFLAIRCSTFORM 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEAITVEVOLPHNFSNRYNRLVRSLLCEDDTVSTIRD 180  
Db 121 IAEVQECYSKLVNCSIAKRNPEAITVEVOLPHNFSNRYNRLVRSLLCEDDTVSTIRD 180  
QY 181 SLMEKIGPMNASLPHILQTDHCQOTHPRADFNRRRTNEPOKLVLLRNLRGEEDESPSHIK 240  
Db 181 SLMEKIGPMNASLPHILQTDHCQOTHPRADFNRRRTNEPOKLVLLRNLRGEEDESPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 3  
US-08-460-529B-10  
; Sequence 10, Application US/08460529B  
; Patent No. 5994103  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Human stannicalcin-alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,529B  
; FILING DATE: June 2, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/13206  
; FILING DATE: 10 NOV 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-08-460-529B-10

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLQNSAVLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
Db 1 MLQNSAVLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
QY 61 ENSTCTDGMWDICKSFLYSAAKFDIOGKAFVKSILKCIANGVTSKVFLAIRCSTFORM 120  
Db 61 ENSTCTDGMWDICKSFLYSAAKFDIOGKAFVKSILKCIANGVTSKVFLAIRCSTFORM 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEAITVEVOLPHNFSNRYNRLVRSLLCEDDTVSTIRD 180



Db 121 IAEVQECYCKLVNCSIAKRNPEALTEVQLPNHFNNRYNRLVRSLLGCEEDSPSHIK 180  
Qy 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVLLRNLRGCEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVLLRNLRGCEEDSPSHIK 240  
Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 4  
US-08-431-117A-2  
; Sequence 2, Application US/08431117A  
; Patent No. 5994301  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannicalcain  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431,117A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,005  
; FILING DATE: 8 MARCH 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-296  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SFO ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVIVISASATHEAEONDSVSPKRSRYAQAQNSAEVVRCLNSALQVCGAFACL 60  
Db 1 MLQNSAVLLVIVISASATHEAEONDSVSPKRSRYAQAQNSAEVVRCLNSALQVCGAFACL 60  
Qy 61 ENSTCDTGMWDICSFYSAKFPDQGAFFVESLKCIANGVTSKVFLAIRCSTFORM 120  
Db 61 ENSTCDTGMWDICSFYSAKFPDQGAFFVESLKCIANGVTSKVFLAIRCSTFORM 120  
Qy 121 IAEVQECYCKLVNCSIAKRNPEALTEVQLPNHFNNRYNRLVRSLLGCEEDSPSHIK 180  
Db 121 IAEVQECYCKLVNCSIAKRNPEALTEVQLPNHFNNRYNRLVRSLLGCEEDSPSHIK 180  
Qy 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVLLRNLRGCEEDSPSHIK 240

Db 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVLLRNLRGCEEDSPSHIK 240  
Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 5  
US-09-361-736B-10  
; Sequence 10, Application US/09361736B  
; Patent No. 6613877  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Stannicalcain-Alpha  
; FILE REFERENCE: PFI43PDI  
; CURRENT APPLICATION NUMBER: US/09/361,736B  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: 08/460,529  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: PCT/ US94/13206  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: human  
; US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVIVISASATHEAEONDSVSPKRSRYAQAQNSAEVVRCLNSALQVCGAFACL 60  
Db 1 MLQNSAVLLVIVISASATHEAEONDSVSPKRSRYAQAQNSAEVVRCLNSALQVCGAFACL 60  
Qy 61 ENSTCDTGMWDICSFYSAKFPDQGAFFVESLKCIANGVTSKVFLAIRCSTFORM 120  
Db 61 ENSTCDTGMWDICSFYSAKFPDQGAFFVESLKCIANGVTSKVFLAIRCSTFORM 120  
Qy 121 IAEVQECYCKLVNCSIAKRNPEALTEVQLPNHFNNRYNRLVRSLLGCEEDSPSHIK 180  
Db 121 IAEVQECYCKLVNCSIAKRNPEALTEVQLPNHFNNRYNRLVRSLLGCEEDSPSHIK 180  
Qy 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVLLRNLRGCEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVLLRNLRGCEEDSPSHIK 240  
Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 6  
US-08-208-005C-5  
; Sequence 5, Application US/08208005C  
; Patent No. 5837498  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannicalcain  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE

Query Match	52.1%;	Score 660.5;	DB 2;	Length 204;
Best Local Similarity	60.8%;	Pred. No. 3.4e-67;		
Matches 118;	Conservative	38;	Mismatches 37;	Indels 1;
				Gaps 1

RESULT 7  
3-09-038-597A-5

APPLICATION NUMBER: US/09/038,597A  
FILING DATE:  
CLASSIFICATION:

Query Match	52.1%;	Score 660.5;	DB 2;	Length 204;
Best Local Similarity	60.8%;	Pred. No. 3.4e-67;		
Matches 118;	Conservative 38;	Mismatches 37;	Indels 1;	Gaps 1;

RESULT 8  
S-08-460-529B-9  
10/24/2008 10:00 AM

REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-334 (PF143)  
TELECOMMUNICATION INFORMATION:



NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/416,150  
FILING DATE: 11-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/831,132  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 96-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6672  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 296 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-416-150-14  
Query Match 28.0%; Score 354.5; DB 3; Length 296;  
Best Local Similarity 31.7%; Pred. No. 5.9e-32;  
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;  
QY 7 LVLVVTSASATHEAEONDSVSP-----RKSVVAQNSAEVVRCLNSALQVGGCA 56  
DB 10 VTLALV--ATLDPAGQSTDTNPPEGFQDRSSQCKGRLSLQNTAEIQHCLVNAQGVGCV 67  
QY 57 FACLENSTCDTDGMYDICKSEFLYSAAKFTQGA FVKESELCIANGVTSKVFLAIRRCSPT 116  
DB 68 FEECENNSCIEQIHGICMTFLHNAKGFDAGKSFIDALRCVHALRHFGCISRKCPA 127  
QY 117 FORMIAVEBECYSKLVNCSIAKRNPEALTEVYQLPNHFNSRYNRLVRSLLCEDEDTVS 176  
DB 128 IREWVFLQRRBCYKHLKDLCSAAQENVIVEMIFPKDLLHEPYVDLVNLLTGSEVKE 187  
QY 177 TIRSLMEKIGPMNASLFHIL-----QTDHCAQTH---PRADFNRRTNEPQKLV 224  
DB 188 AVTSTVQAQCEQSGVGCISLISFCTSNIGRPPTAPRHPGLADRAQLSRPHHRTDTHHL 247  
QY 225 LLRLNLGEEDESPSHIK-----RTSHESA 247  
DB 248 ANRGAKGERGSKSHPNNAHARGRTGGGA 275  
RESULT 12  
US-08-831-132-2  
Sequence 2, Application US/08831132  
GENERAL INFORMATION:  
APPLICANT: Kuestner, Rolf E.  
APPLICANT: Conklin, Darrell C.  
APPLICANT: Lok, Si  
APPLICANT: Buddie, Michele  
APPLICANT: Downey, William  
TITLE OF INVENTION: STANNIOCALCIN-2  
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/831,132  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 96-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6672  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 302 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-831-132-2  
Query Match 27.9%; Score 354; DB 3; Length 302;  
Best Local Similarity 32.4%; Pred. No. 6.9e-32;  
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;  
QY 9 LVLVIS-----ASATHEAE-QNDSVSPKRSVVAQNSAEVVRCLNSALQVGGCA 60  
DB 12 LALVATATDPARGTDATNPPEGFQDRSSQCKGRLSLQNTAEIQHCLVNAQGVGVECF 71  
QY 61 ENSTCDTDGMYDICKSEFLYSAAKFTQGA FVKESELCIANGVTSKVFLAIRRCSPTQRM 120  
DB 72 ENNSCEIRHIGICMTFLHNAKGFDAGKSFIDALRCVHALRHFGCISRKCPAIREM 131  
QY 121 IASVQEBECYSKLVNCSIAKRNPEALTEVYQLPNHFNSRYNRLVRSLLCEDEDTVS 180  
DB 132 VSQQRRECYLGHDCAAQENTRVIVEMIFPKDLLHEPYVDLVNLLTGSEVKEAITH 191  
QY 181 SLMEKIGPMNASLFHILQ-TDHCQTHPRADFNRRTNEPQK----- 222  
DB 192 SVQVQCEQSGVGCISLISFCTSAIQKPTAPRHPGLADRAQLSRPHHRTDTHHLPEPSS 251  
QY 223 KVLRLNLGEEDESPSH 238  
DB 252 RETGRGAKGERGSKSH 267  
RESULT 13  
US-09-416-150-2  
Sequence 2, Application US/09416150  
Patent No. 6171822  
GENERAL INFORMATION:  
APPLICANT: Kuestner, Rolf E.  
APPLICANT: Conklin, Darrell C.  
APPLICANT: Lok, Si  
APPLICANT: Buddie, Michele  
APPLICANT: Downey, William  
TITLE OF INVENTION: STANNIOCALCIN-2  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA

Tue Nov 23 09:18:28 2004

us-09-705-500a-3.ra1

Page 7

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; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6678
; TELEFAX: 206-442-6672
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-416-150-2

Query Match      27.9%; Score 354; DB 3; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKRSRYAQAQNSAEVAVRCINSALOYGCGAFACL 60
DB 12 LALVLAIFDPARGTDATNPBGPDSSQKGRSLQNTAEIQHCLVNAAGVGGVFECE 71
QY 61 ENSTCDTGMVDICKSFLYSAAKFDTOGKAFVKSLSKCIANGVTSKYFLAIRCSTFGQM 120
DB 72 ENNSCEIRGLHGICMTPLHNAKGFDAQGSFIDALCKAHALRHRCGCSRCPAIREM 131
QY 121 IAEVQEECYSKLVNCSIAKRNPEAITTEVQQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 132 VSQLORECYLKHDDCAAAQENTRVIVEMHFKDILLHEPYDVLNLLTTCGEVYKALITH 191
QY 181 SLMEKIGPNMASLPHILQ-TDHCQCTHPRADFNRRRTNEPOKL----- 222
DB 192 SVQVQCEQNMWSLSLSFCTSAIQKPEPTAPPERQPOVDRTKLSRAHGHGHHLPBPSS 251
QY 223 KVLRLNLRGEEDSPSH 238
DB 252 RETGRGAKGERGSKSH 267

RESULT 14
US-09-193-881-23
; Sequence 23, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klases
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: 6248 US P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; CURRENT FILING DATE: 1998-11-18
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; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-881-23

Query Match      27.9%; Score 354; DB 4; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKRSRYAQAQNSAEVAVRCINSALOYGCGAFACL 60
DB 12 LALVLAIFDPARGTDATNPBGPDSSQKGRSLQNTAEIQHCLVNAAGVGGVFECE 71
QY 61 ENSTCDTGMVDICKSFLYSAAKFDTOGKAFVKSLSKCIANGVTSKYFLAIRCSTFGQM 120
DB 72 ENNSCEIRGLHGICMTPLHNAKGFDAQGSFIDALCKAHALRHRCGCSRCPAIREM 131
QY 121 IAEVQEECYSKLVNCSIAKRNPEAITTEVQQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 132 VSQLORECYLKHDDCAAAQENTRVIVEMHFKDILLHEPYDVLNLLTTCGEVYKALITH 191
QY 181 SLMEKIGPNMASLPHILQ-TDHCQCTHPRADFNRRRTNEPOKL----- 222
DB 192 SVQVQCEQNMWSLSLSFCTSAIQKPEPTAPPERQPOVDRTKLSRAHGHGHHLPBPSS 251
QY 223 KVLRLNLRGEEDSPSH 238
DB 252 RETGRGAKGERGSKSH 267

RESULT 15
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; Sequence 12, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stemlocalcin-Alpha
; FILE REFERENCE: PFI43PDI
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-12

Query Match      27.9%; Score 354; DB 4; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKRSRYAQAQNSAEVAVRCINSALOYGCGAFACL 60
DB 12 LALVLAIFDPARGTDATNPBGPDSSQKGRSLQNTAEIQHCLVNAAGVGGVFECE 71
QY 61 ENSTCDTGMVDICKSFLYSAAKFDTOGKAFVKSLSKCIANGVTSKYFLAIRCSTFGQM 120
DB 72 ENNSCEIRGLHGICMTPLHNAKGFDAQGSFIDALCKAHALRHRCGCSRCPAIREM 131
QY 121 IAEVQEECYSKLVNCSIAKRNPEAITTEVQQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 132 VSQLORECYLKHDDCAAAQENTRVIVEMHFKDILLHEPYDVLNLLTTCGEVYKALITH 191
QY 181 SLMEKIGPNMASLPHILQ-TDHCQCTHPRADFNRRRTNEPOKL----- 222
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Db 192 SVQVQCEQNWGSLCSILSFCISAIQKPTAPPERQPOVDRTKUSRAHGEAGHLPSPSS 251  
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Db 252 RETGRGAKGERGSKSH 267

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Job time : 30 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2004, 17:56:22 ; Search time 83 Seconds  
(Without alignments)  
1053.850 Million cell updates/sec

Title: US-09-705-500A-3  
Perfect score: 1268  
Sequence: 1 MGNASVLLVIVISASATHE.....NLNGEEDSPSHIKWTSHESA 247

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	100.0	247	US-09-840-989A-2	Sequence 2, Appl1
2	1268	100.0	247	US-09-361-736-10	Sequence 10, Appl1
3	1268	100.0	247	US-10-116-051-2	Sequence 2, Appl1
4	1268	100.0	247	US-10-177-293-441	Sequence 441, Appl1
5	1268	100.0	247	US-10-418-226-10	Sequence 10, Appl1
6	1268	100.0	247	US-10-465-572-18	Sequence 18, Appl1
7	1268	100.0	247	US-10-372-683-41	Sequence 41, Appl1
8	1268	100.0	247	US-10-614-990-2	Sequence 2, Appl1
9	937	73.9	276	US-09-925-300-1426	Sequence 1426, Appl1
10	662.5	52.2	256	US-09-840-989A-3	Sequence 3, Appl1
11	662.5	52.2	256	US-10-614-990-3	Sequence 3, Appl1
12	660.5	52.1	204	US-10-116-051-10	Sequence 10, Appl1
13	628	49.5	170	US-09-361-736-9	Sequence 9, Appl1

14	628	49.5	170	14	US-10-418-226-9	Sequence 9, Appl1
15	358	28.2	70	9	US-09-864-761-37770	Sequence 37770, A
16	354	27.9	302	9	US-09-193-881-23	Sequence 23, Appl1
17	354	27.9	302	14	US-10-177-293-443	Sequence 443, Appl1
18	354	27.9	302	14	US-10-338-395-23	Sequence 23, Appl1
19	354	27.9	302	14	US-10-418-226-12	Sequence 12, Appl1
20	354	27.9	302	14	US-10-364-889-4	Sequence 4, Appl1
21	354	27.9	302	14	US-10-295-027-100	Sequence 100, Appl1
22	354	27.9	302	15	US-10-173-999-80	Sequence 80, Appl1
23	354	27.9	302	15	US-10-058-370A-22	Sequence 22, Appl1
24	351.5	27.7	251	14	US-10-418-226-2	Sequence 2, Appl1
25	333.5	26.3	251	14	US-09-361-736-2	Sequence 2, Appl1
26	303	23.9	118	13	US-10-116-051-9	Sequence 9, Appl1
27	95.5	7.5	299	15	US-10-282-122A-49895	Sequence 49895, A
28	94.5	7.5	415	17	US-10-425-115-320042	Sequence 320042, A
29	92	7.3	1010	17	US-10-425-115-312927	Sequence 312927, A
30	91	7.2	901	10	US-09-828-062-8	Sequence 8, Appl1
31	91	7.2	901	16	US-10-768-511-8	Sequence 8, Appl1
32	90.5	7.1	783	15	US-10-149-510-96	Sequence 96, Appl1
33	90	7.1	281	11	US-09-973-278-172	Sequence 172, Appl1
34	90	7.1	281	11	US-09-973-278-277	Sequence 277, Appl1
35	90	7.1	331	15	US-10-264-049-2324	Sequence 2324, Appl1
36	89.5	7.1	622	16	US-10-437-963-161551	Sequence 161551, A
37	89.5	7.1	1123	15	US-10-282-122A-70581	Sequence 70581, A
38	89.5	7.1	10203	16	US-10-681-809-23	Sequence 23, Appl1
39	89	7.0	201	17	US-10-425-115-320050	Sequence 320050, A
40	89	7.0	431	17	US-10-425-115-285165	Sequence 285165, A
41	86	6.8	401	15	US-10-425-114-63193	Sequence 63193, A
42	86	6.8	470	15	US-10-282-122A-54827	Sequence 54827, A
43	86	6.8	500	15	US-10-289-762-299	Sequence 299, Appl1
44	86	6.8	529	17	US-10-425-115-320053	Sequence 320053, A
45	85.5	6.7	564	15	US-10-424-599-272057	Sequence 272057, A

#### ALIGNMENTS

RESULT 1  
US-09-840-989A-2  
; Sequence 2, Application US/09840989A  
; Patent No. US20020042372A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: Stemlocalcin Polynucleotides, Polypeptides, and Methods Based The  
; FILE REFERENCE: PFI0892  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/29432  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,740  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-840-989A-2

Query Match 100.0%; Score 1268; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNASVLLVIVISASATHEAFONDSVPPRSRVAAQNSAEVVRCLNSALQVGCAPACT 60  
DB 1 MGNASVLLVIVISASATHEAFONDSVPPRSRVAAQNSAEVVRCLNSALQVGCAPACT 60  
QY 61 ENSTDPTGMVYDCKSPFYSAKFPDQKAFVKSILKIANGVTSKVFLLRRGSTPORM 120  
DB 61 ENSTDPTGMVYDCKSPFYSAKFPDQKAFVKSILKIANGVTSKVFLLRRGSTPORM 120  
QY 121 INVEVECKSKNVGSIKRNPEAITTEVVOIPNHSNNRYRLVPLIECEDPTVSTRD 180  
DB 121 INVEVECKSKNVGSIKRNPEAITTEVVOIPNHSNNRYRLVPLIECEDPTVSTRD 180

Db 121 IAEVQECYKLVNCSIAKRNPEAITVEVOLPNHFSNRYNRLVRSLLCEDEPTVSTIRD 180  
QY 181 SLMEKIGPNMASLPHIIQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEEDSPSHIX 240  
Db 181 SLMEKIGPNMASLPHIIQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEEDSPSHIX 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 2  
US-09-361-736-10  
; Sequence 10, Application US/09361736  
; Patent No. US20020102634A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Human Stamniocalcin-alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/361,736  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/460,529  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-09-361-736-10

Query Match 100.0%; Score 1268; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9, 9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSYPKRSRYAAQNSAEVVRCLNSALQVCGAFACL 60  
Db 1 MLQNSAVLLVVISASATHEAEQNDVSYPKRSRYAAQNSAEVVRCLNSALQVCGAFACL 60  
QY 61 ENSTCDTDGMYDICKSPFLYSAAKFTDQKAFVKSLLKCIANGVTSKVFLLIRRCSTFORM 120  
Db 61 ENSTCDTDGMYDICKSPFLYSAAKFTDQKAFVKSLLKCIANGVTSKVFLLIRRCSTFORM 120  
QY 121 IAEVQECYKLVNCSIAKRNPEAITVEVOLPNHFSNRYNRLVRSLLCEDEPTVSTIRD 180  
Db 121 IAEVQECYKLVNCSIAKRNPEAITVEVOLPNHFSNRYNRLVRSLLCEDEPTVSTIRD 180  
QY 181 SLMEKIGPNMASLPHIIQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEEDSPSHIX 240  
Db 181 SLMEKIGPNMASLPHIIQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEEDSPSHIX 240

Db 181 SLMEKIGPNMASLPHIIQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEEDSPSHIX 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 3  
US-10-116-051-2  
; Sequence 2, Application US/10116051  
; Publication No. US20020146791A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIICALCIN  
; FILE REFERENCE: PFI08PDI01  
; CURRENT APPLICATION NUMBER: US/10/116,051  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 08/431,117  
; PRIOR FILING DATE: 1995-04-28  
; PRIOR APPLICATION NUMBER: 08/208,005  
; PRIOR FILING DATE: 1994-03-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-116-051-2

Query Match 100.0%; Score 1268; DB 13; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9, 9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSYPKRSRYAAQNSAEVVRCLNSALQVCGAFACL 60  
Db 1 MLQNSAVLLVVISASATHEAEQNDVSYPKRSRYAAQNSAEVVRCLNSALQVCGAFACL 60  
QY 61 ENSTCDTDGMYDICKSPFLYSAAKFTDQKAFVKSLLKCIANGVTSKVFLLIRRCSTFORM 120  
Db 61 ENSTCDTDGMYDICKSPFLYSAAKFTDQKAFVKSLLKCIANGVTSKVFLLIRRCSTFORM 120  
QY 121 IAEVQECYKLVNCSIAKRNPEAITVEVOLPNHFSNRYNRLVRSLLCEDEPTVSTIRD 180  
Db 121 IAEVQECYKLVNCSIAKRNPEAITVEVOLPNHFSNRYNRLVRSLLCEDEPTVSTIRD 180  
QY 181 SLMEKIGPNMASLPHIIQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEEDSPSHIX 240  
Db 181 SLMEKIGPNMASLPHIIQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEEDSPSHIX 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 4  
US-10-177-293-441  
; Sequence 441, Application US/10177293  
; Publication No. US20030124128A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Glatz, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Gannavarpu, Manjula  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Mertens, Maureen  
; APPLICANT: Myer, Vic  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Monahan, John  
; APPLICANT: Meyers, Rachel E.



```
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Metic, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 441
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-177-293-441

Query Match          100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKYFLAIRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKYFLAIRCSTFORM 120
QY 121 IAEVQEECYSKLWVCSIAKRNPEAITTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQEECYSKLWVCSIAKRNPEAITTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 5
US-10-418-226-10
; Sequence 10; Application US/10418226
; Publication No. US20030181663A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stemlocalcin-Alpha
; FILE REFERENCE: P143P1D2
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
; US-10-418-226-10

Query Match          100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKYFLAIRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKYFLAIRCSTFORM 120
QY 121 IAEVQEECYSKLWVCSIAKRNPEAITTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQEECYSKLWVCSIAKRNPEAITTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 6
US-10-465-572-18
; Sequence 18; Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Higgins, Gregory
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.00012
; CURRENT APPLICATION NUMBER: US/10/465,572
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201,642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307,600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-465-572-18

Query Match          100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKYFLAIRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKYFLAIRCSTFORM 120
QY 121 IAEVQEECYSKLWVCSIAKRNPEAITTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQEECYSKLWVCSIAKRNPEAITTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
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Db 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGGEEDSPSHIK 240

QY 241 RTSHESA 247  
 241 RTSHESA 247

RESULT 7  
 US-10-372-683-41

; Sequence 41, Application US/10372683  
 ; Publication No. US2004009171A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GERITSEN, MARY E.  
 ; APPLICANT: PEARL JR., FRANKLIN V.  
 ; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOVA  
 ; FILE REFERENCE: P19281P1  
 ; CURRENT APPLICATION NUMBER: US/10/372,683  
 ; CURRENT FILING DATE: 2003-02-21  
 ; PRIOR APPLICATION NUMBER: US 10/271,690  
 ; PRIOR FILING DATE: 2002-10-16  
 ; PRIOR APPLICATION NUMBER: US 60/344,534  
 ; PRIOR FILING DATE: 2001-10-18  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SEQ ID NO 41  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-372-683-41

Query Match 100.0%; Score 1268; DB 15; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 9,9e-121;  
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLONSAYLVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60  
 Db 1 MLONSAYLVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60  
 QY 61 ENSTCDTDGMYDICKSFLYSAKFTQGAFFVESLKCIANGVTSKVFLAIRRCSFTQRM 120  
 Db 61 ENSTCDTDGMYDICKSFLYSAKFTQGAFFVESLKCIANGVTSKVFLAIRRCSFTQRM 120  
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITVEVOLPHNFSNRYNRLVRSLLCEDDVTSTIRID 180  
 Db 121 IAEVQECYSKLVNCSIAKRNPEAITVEVOLPHNFSNRYNRLVRSLLCEDDVTSTIRID 180  
 QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
 Db 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
 QY 241 RTSHESA 247  
 Db 241 RTSHESA 247

RESULT 8

US-10-614-990-2  
 ; Sequence 2, Application US/10614990  
 ; Publication No. US20040198658A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olsen et al.  
 ; TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based TH  
 ; FILE REFERENCE: P1108P2  
 ; CURRENT APPLICATION NUMBER: US/10/614,990  
 ; CURRENT FILING DATE: 2003-07-09  
 ; PRIOR APPLICATION NUMBER: US/09/840,989A  
 ; PRIOR FILING DATE: 2001-04-25  
 ; PRIOR APPLICATION NUMBER: PCT/US00/29432  
 ; PRIOR FILING DATE: 2000-10-26  
 ; PRIOR APPLICATION NUMBER: US 60/161,740  
 ; PRIOR FILING DATE: 1999-10-27  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-614-990-2

Query Match 100.0%; Score 1268; DB 17; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 9,9e-121;  
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLONSAYLVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60  
 Db 1 MLONSAYLVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60  
 QY 61 ENSTCDTDGMYDICKSFLYSAKFTQGAFFVESLKCIANGVTSKVFLAIRRCSFTQRM 120  
 Db 61 ENSTCDTDGMYDICKSFLYSAKFTQGAFFVESLKCIANGVTSKVFLAIRRCSFTQRM 120  
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITVEVOLPHNFSNRYNRLVRSLLCEDDVTSTIRID 180  
 Db 121 IAEVQECYSKLVNCSIAKRNPEAITVEVOLPHNFSNRYNRLVRSLLCEDDVTSTIRID 180  
 QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
 Db 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
 QY 241 RTSHESA 247  
 Db 241 RTSHESA 247

RESULT 9

US-09-925-300-1426  
 ; Sequence 1426, Application US/09925300  
 ; Patent No. US20020151681A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Craig Rosen,  
 ; APPLICANT: Steve Ruben  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA101  
 ; CURRENT APPLICATION NUMBER: US/09/925,300  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/059988  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 1890  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1426  
 ; LENGTH: 276  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURES:  
 ; NAME/KEY: SITE  
 ; LOCATION: (43)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (273)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (275)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-925-300-1426

Query Match 73.9%; Score 937; DB 9; Length 276;  
 Best Local Similarity 99.5%; Pred. No. 6,6e-87;  
 Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLONSAYLVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60  
 Db 89 MLONSAYLVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 148  
 QY 61 ENSTCDTDGMYDICKSFLYSAKFTQGAFFVESLKCIANGVTSKVFLAIRRCSFTQRM 120

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Db      149 ENSCTDDGMDICKSLFYSAKAFDTQGAFFKESLKCINGVTSKYFLAIRRCSFTQRM 208
QY      121 IAEVQECYSKLVNCSIAKENPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
Db      209 IAEVQECYSKLVNCSIAKENPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 268
QY      181 SIMEXI 186
Db      269 SIMEXI 274
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## RESULT 10

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US-09-840-989A-3
; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/09/840, 989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-09-840-989A-3
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Query Match      52.2%; Score 662.5; DB 9; Length 256;
Best Local Similarity 53.4%; Pred. No. 6e-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;
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QY      11 LVISASATHEAEQNDVSPPKRSRYAQAQNSAEVVRCLNSALQVCGAFACLENSTCTDDGM 70
Db      12 LVIGTAATFTDTPDEA-SPRRARFSSNSPSDVARCLNGALAVGCGTACLENSTCTDDGM 70
QY      71 YDICKSFLYSAKAFDTQGAFFKESLKCINGVTSKYFLAIRRCSFTQRMIAEVQECYS 130
Db      71 HDICQLFHTAATFTQGTFFVKESLRCIANGVTSKYFQTRRCGVGFQRMISSEVQECYS 130
QY      131 KLVNCSIAKENPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRDSIMEKIGPNM 190
Db      131 RLDICGVARSNPEAIGEVVQVPAHPNRYYSTLLQSLACDEETVAVVRAGLVARLGPDM 190
QY      191 ASLFHILQTDHCAQTHPRADFN---RRRTNEPQKLKVLRLNRGSEEDSPSHI 239
Db      191 ETLFOLLQNKHCPOGSGNCPNSAPAGWRWPMGSPSPFKI-QPSMRGRD--PTHL 241
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## RESULT 11

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US-10-614-990-3
; Sequence 3, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/10/614, 990
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840, 989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-614-990-3
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Query Match      52.2%; Score 662.5; DB 17; Length 256;
Best Local Similarity 53.4%; Pred. No. 6e-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;
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QY      11 LVISASATHEAEQNDVSPPKRSRYAQAQNSAEVVRCLNSALQVCGAFACLENSTCTDDGM 70
Db      12 LVIGTAATFTDTPDEA-SPRRARFSSNSPSDVARCLNGALAVGCGTACLENSTCTDDGM 70
QY      71 YDICKSFLYSAKAFDTQGAFFKESLKCINGVTSKYFLAIRRCSFTQRMIAEVQECYS 130
Db      71 HDICQLFHTAATFTQGTFFVKESLRCIANGVTSKYFQTRRCGVGFQRMISSEVQECYS 130
QY      131 KLVNCSIAKENPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRDSIMEKIGPNM 190
Db      131 RLDICGVARSNPEAIGEVVQVPAHPNRYYSTLLQSLACDEETVAVVRAGLVARLGPDM 190
QY      191 ASLFHILQTDHCAQTHPRADFN---RRRTNEPQKLKVLRLNRGSEEDSPSHI 239
Db      191 ETLFOLLQNKHCPOGSGNCPNSAPAGWRWPMGSPSPFKI-QPSMRGRD--PTHL 241
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## RESULT 12

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US-10-116-051-10
; Sequence 10, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: COSPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PFI08P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-116-051-10
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Query Match      52.1%; Score 660.5; DB 13; Length 204;
Best Local Similarity 60.8%; Pred. No. 7e-59;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;
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QY      11 LVISASATHEAEQNDVSPPKRSRYAQAQNSAEVVRCLNSALQVCGAFACLENSTCTDDGM 70
Db      12 LVIGTAATFTDTPDEA-SPRRARFSSNSPSDVARCLNGALAVGCGTACLENSTCTDDGM 70
QY      71 YDICKSFLYSAKAFDTQGAFFKESLKCINGVTSKYFLAIRRCSFTQRMIAEVQECYS 130
Db      71 HDICQLFHTAATFTQGTFFVKESLRCIANGVTSKYFQTRRCGVGFQRMISSEVQECYS 130
QY      131 KLVNCSIAKENPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRDSIMEKIGPNM 190
Db      131 RLDICGVARSNPEAIGEVVQVPAHPNRYYSTLLQSLACDEETVAVVRAGLVARLGPDM 190
QY      191 ASLFHILQTDHCAQ 204
Db      191 ETLFOLLQNKHCPO 204
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## RESULT 13



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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37770
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012119.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUE 3.00e-35
; OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUE 3.00e-34
US-09-864-761-37770

Query Match          28.2%; Score 358; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      88  GKAFVKESLKCICANGVTSTKVFLAIRRCSTFORMIAEYQEECYSKLNVCSIAKKNPEAITE 147
      1  GKAFVKESLKCICANGVTSTKVFLAIRRCSTFORMIAEYQEECYSKLNVCSIAKKNPEAITE 60
      148  VVQLENHFSN 157
      61  VVQLENHFSN 70
      Db
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Search completed: November 22, 2004, 18:11:16  
Job time : 86 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2004, 16:07:12 ; Search time 377 Seconds  
(without alignments)  
7209.609 Million cell updates/sec

Title: US-09-705-500A-1

Perfect score: 1 ctataatgcttctacataa.....taataagtgctacgtttta 503

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 362788 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
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19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	503	100.0	3765	13	US-10-044-090-638
2	503	100.0	3897	14	US-10-198-846-13651
3	458	91.1	3757	16	US-10-641-643-1502
4	458	91.1	3901	15	US-10-177-293-440
5	458	91.1	3901	15	US-10-465-572-117
6	458	91.1	3901	16	US-10-159-563-292
7	458	91.1	3901	16	US-10-372-683-40
8	458	91.1	3901	16	US-10-240-425-1425
9	393.4	78.2	572	16	US-10-152-319A-1327
10	229.4	44.7	263	9	US-09-880-107-249
11	224.8	44.7	563	10	US-09-814-353-18293
12	209.6	41.7	390	10	US-09-814-353-5622

13	209.6	41.7	390	10	US-09-814-353-11909	Sequence 11909, A
14	176.8	35.1	556	15	US-10-102-524-873	Sequence 873, App
15	60	11.9	60	10	US-09-908-975-1768	Sequence 1768, A
16	60	11.9	60	10	US-09-908-975-1919	Sequence 1919, A
17	55.8	11.1	3673778	15	US-10-312-841-2	Sequence 2, App1
18	53.4	11.0	6917	15	US-10-311-455-208	Sequence 208, App
19	55	10.9	12237	15	US-10-311-455-2331	Sequence 2331, App
20	54.8	10.9	19087	15	US-10-311-455-766	Sequence 766, App
21	54.6	10.9	6154	16	US-10-221-653-79	Sequence 69, App1
22	53.6	10.7	5689	14	US-10-239-676-90	Sequence 90, App1
23	53.6	10.7	5689	15	US-10-240-453-100	Sequence 100, App
24	53.6	10.7	5689	16	US-10-221-724A-148	Sequence 148, App
25	53.4	10.6	8254	15	US-10-311-455-837	Sequence 837, App
26	53.4	10.6	17234	17	US-10-433-793-88	Sequence 48, App1
27	52.6	10.5	10328	15	US-10-311-455-1517	Sequence 1517, App
28	51.2	10.2	10133	15	US-10-311-455-432	Sequence 432, App
29	51.2	10.2	37515	17	US-10-433-793-28	Sequence 28, App1
30	51.2	10.2	3673778	15	US-10-312-841-1	Sequence 1, App1
31	51	10.1	15479	16	US-10-257-166-45	Sequence 45, App1
32	50.8	10.1	5829	15	US-10-311-455-1700	Sequence 1700, App
33	50.8	10.1	6074	15	US-10-311-455-1038	Sequence 1038, App
34	50.8	10.1	8592	15	US-10-311-455-1955	Sequence 1955, App
35	50.6	10.1	15518	15	US-10-311-455-2145	Sequence 2145, App
36	50.6	10.1	15518	15	US-10-240-485-177	Sequence 177, App
37	50.4	10.0	5107	15	US-10-311-455-1039	Sequence 1039, App
38	50.4	10.0	14924	15	US-10-311-455-198	Sequence 198, App
39	50.4	10.0	14924	15	US-10-240-452-42	Sequence 22, App1
40	50.2	10.0	9741	15	US-10-311-455-1296	Sequence 1296, App
41	50.2	10.0	16688	15	US-10-311-455-293	Sequence 293, App
42	49.8	9.9	5291	15	US-10-311-455-1292	Sequence 1292, App
43	49.8	9.9	5291	15	US-10-240-452-58	Sequence 58, App1
44	49.6	9.9	6092	15	US-10-221-613-36	Sequence 36, App1
45	49.6	9.9	6352	15	US-10-172-086-23	Sequence 23, App1

ALIGNMENTS

RESULT 1  
US-10-044-090-638  
; Sequence 638, Application US/10044090  
; Publication No. US20020137081A1  
; GENERAL INFORMATION:  
; APPLICANT: Oiga Bandman  
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
; FILE REFERENCE: PA-0028 US  
; CURRENT APPLICATION NUMBER: US/10/044.090  
; CURRENT FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: PERL Program  
; SEQ ID NO 638  
; LENGTH: 3765  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Inocyte ID No. US20020137081A1 33181.1  
; LOCATION: 2378..3184..3187..3194  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-044-090-638  
Query Match 100.0%; Score 503; DB 13; Length 3765;  
Best Local Similarity 100.0%; Pred. No. 1e-101;  
Matches 503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTATTATGCTATCTTCACATATATCTTACACATAGAGAAAGAGAGCTTCTACATG 60  
DB 3255 CTATTATGCTATCTTCACATATATCTTACACATAGAGAAAGAGAGCTTCTACATG 3314  
QY 61 TTGCTAGTTTTCCTTCTCTTCCACACCTTCCTCCATTCCTCCCTTAACTTC 120  
DB 3315 TTGCTAGTTTTCCTTCTCTTCCACACCTTCCTCCATTCCTCCCTTAACTTC 3374





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CLONE: g975297
SEQUENCE DESCRIPTION: SEQ ID NO: 1502 :
US-10-641-643-1502

Query Match      91.1%; Score 458; DB 16; Length 3757;
Best Local Similarity 99.2%; Pred. No. 1e-91;
Matches 502; Conservative 0; Mismatches 0; Indels 4; Gaps 4;

QY 1 CTATATATGATCTACATACATATATCTACACATACAGAAAGAGAGAGTCTACAAATG 60
DB 3244 CTATATATGATCTACATACATATATCTACACATACAGAAAGAGAGAGTCTACAAATG 60
QY 61 TTGGTATGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 119
DB 3303 TTGGTATGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 119
QY 120 CCAAGCTTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 179
DB 3363 CCAAGCTTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 179
QY 180 ATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239
DB 3423 ATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239
QY 240 TATGATTTTAAATTAATGATATTTAGGTTTTTGGCTGAGTACTGGAATTAACAGTGA 239
DB 3483 TATGATTTTAAATTAATGATATTTAGGTTTTTGGCTGAGTACTGGAATTAACAGTGA 239
QY 300 GCATATCTGATATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 358
DB 3543 GCATATCTGATATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 358
QY 359 ATAAAGCTTGAAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
DB 3603 ATAAAGCTTGAAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
QY 418 TTATTAATTAAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
DB 3663 TTATTAATTAAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
QY 478 AAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 503
DB 3723 AAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 503

RESULT 4
US-10-177-293-440
Sequence 440, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatz, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavarapu, Manjula
APPLICANT: Kamatkar, Shubhang
APPLICANT: Mertens, Maureen
APPLICANT: Meyer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Baet Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
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PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 440
LENGTH: 3901
TYPE: DNA
ORGANISM: Homo sapiens
US-10-177-293-440

Query Match      91.1%; Score 458; DB 15; Length 3901;
Best Local Similarity 99.2%; Pred. No. 1.e-91;
Matches 502; Conservative 0; Mismatches 0; Indels 4; Gaps 4;

QY 1 CTATATGATCTACATACATATATCTACACATACAGAAAGAGAGAGTCTACAAATG 60
DB 3363 CTATATGATCTACATACATATATCTACACATACAGAAAGAGAGAGTCTACAAATG 60
QY 61 TTGGTATGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 119
DB 3428 TTGGTATGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 119
QY 120 CCAAGCTTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 179
DB 3488 CCAAGCTTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 179
QY 180 ATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239
DB 3548 ATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239
QY 240 TATGATTTTAAATTAATGATATTTAGGTTTTTGGCTGAGTACTGGAATTAACAGTGA 299
DB 3608 TATGATTTTAAATTAATGATATTTAGGTTTTTGGCTGAGTACTGGAATTAACAGTGA 299
QY 300 GCATATCTGATATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 358
DB 3668 GCATATCTGATATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 358
QY 359 ATAAAGCTTGAAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
DB 3728 ATAAAGCTTGAAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
QY 418 TTATTAATTAAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
DB 3788 TTATTAATTAAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
QY 478 AAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 503
DB 3848 AAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 503

RESULT 5
US-10-465-572-17
Sequence 17, Application US/10465572
Publication No. US20030207840A1
GENERAL INFORMATION:
APPLICANT: Higgins, Gregory
APPLICANT: Lal, Anita
TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
FILE REFERENCE: 000250.00012
CURRENT APPLICATION NUMBER: US/10/465,572
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/10/201,642
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QY		CTATATATGATCTATCAACATATACATATATCTACACATACAGAAAGAGAGCTCTACAAATG	60
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QY	61	TTGCTAGATTTTGTGCTTCTCTTTGCCCCACCCCTACTCCCTCCCAAT-CCCCCTTAAACTT	119
Db	3428	TTGCTAGATTTTGTGCTTCTCTTTGCCCCACCCCTACTCCCTCCCAATCCCCCTTAAACTT	3487
QY	120	CCAAAGCTTCGCTCTGTGTGTGTGCTGCAGAGATGATTCGGGGGCTGACCTTACACCACTTTCG	179
Db	3488	CCAAAGCTTCGCTCTGTGTGTGTGCTGCAGAGATGATTCGGGGGCTGACCTTACACCACTTTCG	3547
QY	180	ATGATTTCTTCTCTGTGATTTGGTTGGTGCACCTTAAACATTTTGTGCCATTTATATTTGCAT	239
Db	3548	ATGATTTCTTCTCTGTGATTTGGTTGGTGCACCTTAAACATTTTGTGCCATTTATATTTGCAT	3607
QY	240	TATGATTTTATTAATTAATTAATGATATTTTATGTTTTTGGCTGAGTACTGGAATTAACATGA	299
Db	3608	TATGATTTTATTAATTAATTAATGATATTTTATGTTTTTGGCTGAGTACTGGAATTAACATGA	3667
QY	300	GCAATATCTGATATATGTCATATATTTATTTGCTAAATTTACA-TTTTAAAGCTCCAGTGCAT	358
Db	3668	GCAATATCTGATATATGTCATATATTTATTTGCTAAATTTATACATTTTAAAGCTCCAGTGCAT	3727
QY	359	ATAAAGGTTATGAACAATATCATGTGTAATGACAGATGCAGTCACTTATTTATTTGCTTA-TT	417
Db	3728	ATAAAGGTTATGAACAATATCATGTGTAATGACAGATGCAGTCACTTATTTATTTGCTTATTT	3787
QY	418	TTTATTAATTAAGATGCGCATGCAATATATATGAGCGCTTGTGTAATCTCTCTTAAGATTA	477
Db	3788	TTTATTAATTAAGATGCGCATGCAATATATATGAGCGCTTGTGTAATCTCTCTTAAGATTA	3847
QY	478	AAATTAATTAATAAGTGTACGTTTTA 503	
Db	3848	AAATTAATTAATAAGTGTACGTTTTA 3873	
RESULT 7			
US-10-372-683-40			
/ Sequence 40, Application US/10372683			
/ Publication No. US20040009171A1			
GENERAL INFORMATION:			
/ APPLICANT: GERRITSEN, MARY E.			
/ APPLICANT: PEALE JR., FRANKLIN V.			
/ APPLICANT: WU, THOMAS D.			
/ TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA			
/ FILE REFERENCE: PI92881P1			
/ CURRENT APPLICATION NUMBER: US/10/372,683			
/ CURRENT FILING DATE: 2003-02-21			
/ PRIOR APPLICATION NUMBER: US 10/271,690			
/ PRIOR FILING DATE: 2002-10-16			
/ PRIOR APPLICATION NUMBER: US 60/344,534			
/ PRIOR FILING DATE: 2001-10-18			
/ NUMBER OF SEQ ID NOS: 49			
/ SEQ ID NO. 40			
/ LENGTH: 3901			
/ TYPE: DNA			
/ ORGANISM: Homo sapien			
US-10-372-683-40			

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Db 3369 CTATATATGTATCTACAAATACATATATATCTACATACAGAAAGAGCTTCTAC-ATG 3427
Qy 61 TTGCTAGTTTTTGGCTCTCTTCCGCCACCTTACCTCCCAATT-CCCCCTTAACTT 119
Db 3428 TTGCTAGTTTTTGGCTCTCTTCCGCCACCTTACCTCCCAATTCCCCCTTAACTT 3487
Qy 120 CCAAGCTTGGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 179
Db 3488 CCAAGCTTGGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3547
Qy 180 ATGATCTCTCTGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 239
Db 3548 ATGATCTCTCTGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3607
Qy 240 TATGATTTATTAATTAATGATTTAGTTTTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 299
Db 3608 TATGATTTATTAATTAATGATTTAGTTTTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3667
Qy 300 GCATATCTGCTGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 358
Db 3668 GCATATCTGCTGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3727
Qy 359 ATAAAGTTATGAAACATATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 417
Db 3728 ATAAAGTTATGAAACATATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3787
Qy 418 TTATTAATTAAGATGCTGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 477
Db 3788 TTATTAATTAAGATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3847
Qy 478 AAATTAATTAAGATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 503
Db 3848 AAATTAATTAAGATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3873
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## RESULT 8

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US-10-240-425-1425
; Sequence 1425, Application US/10240425
; Publication No. US2004003502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scheff, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1425
; LENGTH: 3901
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US2004003502A1 U25997
US-10-240-425-1425
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Query Match 91.1%; Score 458; DB 16; Length 3901;
Best Local Similarity 99.2%; Pred. No. 1,1e-91;
Matches 502; Conservative 0; Mismatches 0; Indels 4; Gaps 4;
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Qy 1 CTATATATGTATCTACAAATACATATATCTACATACAGAAAGAGCTTCTACAAAGT 60
Db 3369 CTATATATGTATCTACAAATACATATATCTACATACAGAAAGAGCTTCTAC-ATG 3427
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Qy 61 TTGCTAGTTTTTGGCTCTCTTCCGCCACCTTACCTCCCAANT-CCCCCTTAACTT 119
Db 3428 TTGCTAGTTTTTGGCTCTCTTCCGCCACCTTACCTCCCAANTCCCCCTTAACTT 3487
Qy 120 CCAAGCTTGGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 179
Db 3488 CCAAGCTTGGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3547
Qy 180 ATGATCTCTCTGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 239
Db 3548 ATGATCTCTCTGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3607
Qy 240 TATGATTTATTAATTAATGATTTAGTTTTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 299
Db 3608 TATGATTTATTAATTAATGATTTAGTTTTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3667
Qy 300 GCATATCTGCTGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 358
Db 3668 GCATATCTGCTGCTGCTGCTTGGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3727
Qy 359 ATAAAGTTATGAAACATATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 417
Db 3728 ATAAAGTTATGAAACATATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3787
Qy 418 TTATTAATTAAGATGCTGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 477
Db 3788 TTATTAATTAAGATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3847
Qy 478 AAATTAATTAAGATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 503
Db 3848 AAATTAATTAAGATGCTGCTGAGAGTATGCGGGGCTGACCTGACCAAGTTGC 3873
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## RESULT 9

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US-10-152-319A-1327/C
; Sequence 1327, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1327
; LENGTH: 572
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; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI235210
US-10-152-319A-1327

Query Match          78.2%; Score 393.4; DB 16; Length 572;
Best Local Similarity 91.5%; Pred. No. 1.2e-77;
Matches 453; Conservative 0; Mismatches 31; Indels 11; Gaps 3;

QY 4 TATATGATCTACAAATACATATATCTTACACATACAGAAAGCAATCTCCCAAGTGG 63
DB 510 TATATGATCAACAATACATATATCTTACACATATGAGAAAGCAATCTCCCAAGTGG 451
QY 64 CTAGTTTCTGCTTCTCTT-----CCCCCACCCTACTCCCTCCCAATCCCTTAA 115
DB 450 CTAGTTTCTGCTTCTCTTCTTCTTCTCCACACCCTCCGCTCTCTCACTCTCTTAA 391
QY 116 ACTTCCAAAGCTTGCTTCTGTTTGTCTGCAAGTGATTTGGGGGCTGACCTAGACCACT 175
DB 390 ACTTCCAAAGCTTCTTCTCTGTTTGTCTGCAAGTGATTTGGGGGCTGACCTAGACCACT 331
QY 176 TTGATATATCTCTCTGTTGATTTGGTTCACCTTTAG-ACATTTTGTGCAATATAT 234
DB 330 TTGCAATAT--CTCTCCGATTTGGTTGCACTTTAGAACATTTTGTGCCCTTATAT 273
QY 235 TGCATATGATTTTATATATTTAAATGATTTAGTTTGGCTGAGTACTGGAAATAAAC 294
DB 272 TGCATATGATTTTATATATTTAAATGATTTAGTTTGGCTGAGTACTGGAAATAAAC 213
QY 295 AGTGAAGATATCTGATATATGCTATTTATTTATTTAGTTAACTTTTAAAGCTCCACT 354
DB 212 AGTGAAGATATCTGATATATGCTATTTATTTATTTATTTTAACTTTTAAAGCTCCACT 153
QY 355 GCATATTAAGGTTATGAAACATATCATGTATGACAGATGCAAGTATTTATTTTGGCT 414
DB 152 GCATATTAAGGTTATGAAACATATCATGTATGACAGATGCAAGTATTTATTTTGGCT 93
QY 415 ATTTTATATTAAGTGCATATGATATATGAAAGCTTGGTGAATTCCTCTCAAA 474
DB 92 ATTTTATATTAAGTGCATATGATATTTGAAAGCTTGGTGAATTCCTCTCAAGA 33
QY 475 TAAAAATATATATTA 489
DB 32 TAAATATATATATTA 18

RESULT 10
US-09-880-107-249/c
; Sequence 249, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Schett, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 249
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA126561
NAME/KEY: unsure
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; LOCATION: (1)..(263)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-249

Query Match          45.6%; Score 229.4; DB 9; Length 263;
Best Local Similarity 95.7%; Pred. No. 2.6e-41;
Matches 244; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 249 ATATTTAAATGATATTTAGTTTGTGGCTGAGTACTGATTAACAAGTACATATCTG 308
DB 263 ATATTTAAATGATATTTAGTTTGTGGCTGAGTACTGANT-AACAGNAGCATATCTG 205
QY 309 GTATATGCTATTTATTTGTTAAATTAATTAATTAAGCTCCATGCAATTAAGTTA 368
DB 204 GTATATGCTATTTATTTGTTAAATTAATTAATTAAGCTCCATGCAATTAAGTTA 145
QY 369 TGAACATATCATGATATGACAGATGCAAGTTATTTATTTGCTTATTTTAAATTA 428
DB 144 TGAACATATCATGATATGACAGATGCAAGTTATTTATTTGCTTATTTTAAATTA 85
QY 429 AGATGCAATGCAATATATATGAGCTTTGGTGAATTCCTTCTAAGATTAATAATA 488
DB 84 AGATGCAATGCAATATATATGAGCTTTGGTGAATTCCTTCTAAGATTAATAATA 25
QY 489 AAGTTTACGTTTAA 503
DB 24 AAGTTTACGTTTAA 10

RESULT 11
US-09-814-353-18293
; Sequence 18293, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-0068
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18293
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 466, 467, 468, 470, 471, 473, 475, 490, 520, 521
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-18293

Query Match          44.7%; Score 224.8; DB 10; Length 563;
Best Local Similarity 99.1%; Pred. No. 3.6e-40;
Matches 226; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 276 GCTGAGTACTGGAATTAACAGTGAATATCTGTATATGCTATTTATTTATTTATTT 335
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Db      228 GGTAGTACTGGAATAAACAAGTACGATATCTGTATATGTCATTTATTTTGTAAATT 287
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5622
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-5622
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RESULT 12
; Sequence 5622, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5622
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-5622
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Query Match      41.7%; Score 209.6; DB 10; Length 390;
Best Local Similarity 97.8%; Pred. No. 7.6e-37;
Matches 223; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

; US-10-102-524-873
; Sequence 873, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Mannion, Jane
; APPLICANT: Gauger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 873
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-11909
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; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11909
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-11909
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Query Match      41.7%; Score 209.6; DB 10; Length 390;
Best Local Similarity 97.8%; Pred. No. 7.6e-37;
Matches 223; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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Qy      276 GCTGAGTACTGGAATAAACAAGTACGATATCTGTATATGTCATTTATTTTGTAAATT 335
Db      163 GGTAGTACTGGAATAAACAAGTACGATATCTGTATATGTCATTTATTTTGTAAATT 222
; US-10-102-524-873
; Sequence 873, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Mannion, Jane
; APPLICANT: Gauger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 873
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-11909
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RESULT 13
; Sequence 11909, Application US/09814353
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FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 327, 343, 510, 543  
OTHER INFORMATION: n = A,T,C or G  
US-102-524-873

Query Match 35.1%; Score 176.8; DB 15; Length 556;  
Best Local Similarity 97.8%; Pred. No. 1.7e-29;  
Matches 178; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTATATATGATCTACATACATATATCTACATACAGAAAGACAGTTCTCACATG 60  
DB 375 CTATATATGATCTACAGTACATATATCTACATACAGAAAGACAGTTCTCACATG 434  
QY 61 TTGCTAGTTTTCCTCTCTTCCGCCACCTACTCCCTCAATCCCTTAACTTC 120  
DB 435 TTGCTAGTTTTCCTCTCTTCCGCCACCTACTCCCTCAATCCCTTAACTTC 494  
QY 121 CAAAGCTCGCTGTTGTTGTCGACAGATTCGGGGCTGACCTAGACCAATTGCA 180  
DB 495 CAAAGCTCGCTGTTGTTGTCGACAGATTCGGGGCTGACCTAGACCAATTGCA 554  
QY 181 TG 182  
DB 555 TG 556

# RESULT 15

US-09-908-975-31768  
Sequence 31768, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: MASSEMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: FAIGLER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31768  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-31768

Query Match 11.9%; Score 60; DB 10; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0.00069;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GTGATTGGGGGCTGACCTAGACCAAGTTGCATGTTCTTCTTGATTTGGTTGAC 208  
DB 1 GTGATTGGGGGCTGACCTAGACCAAGTTGCATGTTCTTCTTGTGATTTGGTTGAC 60

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2\_6/prodata/1/iaa/PCUTS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfillsl.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	8.6	144	2	US-08-950-168-1
2	75	8.6	144	3	US-09-365-705-1
3	75	8.6	144	4	US-09-702-705-327
4	75	8.6	144	4	US-09-736-457-327
5	75	8.6	144	4	US-09-614-124B-327
6	75	8.6	144	4	US-09-671-325-327
7	75	8.6	144	4	US-09-589-184-327
8	75	8.6	144	4	US-09-658-824-327
9	75	8.6	145	4	US-09-257-179-63
10	74.5	8.5	664	4	US-09-823-038A-48
11	72.5	8.2	330	4	US-09-270-767-46166
12	71.5	8.2	353	4	US-09-270-767-34960

13	71.5	8.2	353	4	US-09-270-767-50177	Sequence 50177, A
14	70.5	8.1	63	4	US-09-248-796A-27951	Sequence 27951, A
15	70.5	8.1	405	4	US-09-134-000C-5472	Sequence 5472, A
16	70	8.0	315	4	US-09-248-796A-15178	Sequence 15178, A
17	68	7.8	248	4	US-09-270-767-18407	Sequence 18407, A
18	68	7.8	248	4	US-09-270-767-53624	Sequence 53624, A
19	68	7.8	440	4	US-09-270-767-46800	Sequence 46800, A
20	68	7.7	960	3	US-09-345-650-1	Sequence 1, Appl1
21	67.5	7.7	266	4	US-09-270-767-34032	Sequence 34032, A
22	67.5	7.7	266	4	US-09-270-767-49249	Sequence 49249, A
23	67	7.7	103	4	US-09-270-767-18215	Sequence 38215, A
24	67	7.7	103	4	US-09-270-767-53432	Sequence 53432, A
25	67	7.6	254	4	US-09-586-106D-93	Sequence 93, Appl
26	66.5	7.6	372	4	US-09-668-097A-14	Sequence 14, Appl
27	66	7.6	354	4	US-09-270-767-39281	Sequence 39281, A
28	66	7.6	354	4	US-09-270-767-54498	Sequence 54498, A
29	65.5	7.5	515	3	US-08-796-899-24	Sequence 24, Appl
30	65.5	7.4	587	4	US-09-270-767-37567	Sequence 37567, A
31	65.5	7.4	587	4	US-09-270-767-52784	Sequence 52784, A
32	65	7.4	133	3	US-09-384-162-16375	Sequence 16, Appl
33	65	7.4	149	4	US-09-270-767-43975	Sequence 43975, A
34	65	7.4	237	4	US-09-270-767-40963	Sequence 40963, A
35	65	7.4	237	4	US-09-270-767-56179	Sequence 56179, A
36	65	7.4	716	4	US-09-270-767-42322	Sequence 42322, A
37	64.5	7.3	603	2	US-08-687-865A-2	Sequence 2, Appl1
38	64.5	7.3	603	3	US-09-043-711-2	Sequence 210, Appl
39	64.5	7.4	677	4	US-10-140-002-230	Sequence 6555, Ap
40	64	7.2	206	4	US-09-543-681A-6555	Sequence 15999, A
41	64	7.2	239	4	US-09-248-796A-11599	Sequence 41529, A
42	64	7.2	513	4	US-09-270-767-11529	Sequence 36669, A
43	63.5	7.2	153	4	US-09-270-767-11866	Sequence 51866, A
44	63.5	7.2	153	4	US-09-270-767-11866	Sequence 20444, A
45	63.5	7.3	228	4	US-09-248-796A-20444	

## ALIGNMENTS

RESULT 1  
US-08-950-168-1  
; Sequence 1, Application US/08950168  
; Patent No. 5968744  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN CORNICHO PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/950,168  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0401 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166

TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 144 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BLADNOT04  
CLONE: 1318847  
US-08-950-168-1

Alignment Scores:  
Pred. No.: 0.153 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9

US-09-705-500a-1 (1-503) x US-08-950-168-1 (1-144)

QY 142 CTGCAAGTATTCGGGGGCTGACCTAGACCACTTGCATGATTCCTCTTGATTTG 201  
|||:|||||  
Db 34 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 47  
|||:|||||  
QY 202 -----CTGCACCTTGAACATTTTGTGCCAT---TATATTGCATTAGATTTA 249  
|||:|||||  
Db 48 LeuAsnProLeuValLeuProGluTyrLeuIleHisAlaPheMetCysValMetPheLeu 67  
|||:|||||  
QY 250 TAATTAAATGATATTAGTTTGGCTGAGTACTGCAATAAAC-----AGT 297  
|||:|||||  
Db 68 -----CysAlaIleAlaGluTyrPheuThrLeuGlyLeuAsnMetProLeuLeuAla 83  
|||:|||||  
QY 298 GAGCATATCTGG---TATATGTCA----- 318  
|||:|||||  
Db 84 TyrHisIleTyrArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103  
|||:|||||  
QY 319 TTATTATGTTAAATTACATTTTAAAGCTCCATGTCATATAAAGTTATGAACATAT 378  
|||:|||||  
Db 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGluGlyTyr----- 120  
|||:|||||  
QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420  
|||:|||||  
Db 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130  
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RESULT 2  
US-09-365-705-1  
Sequence 1, Application US/09365705  
Patent No. 6348576  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
Corley, Neil C.  
Shah, Purvi  
TITLE OF INVENTION: HUMAN CORNICHON PROTEIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/365,705  
FILING DATE: 02-Aug-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/950,168

FILING DATE: 14-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0401 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 144 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BLADNOT04  
CLONE: 1318847  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-365-705-1

Alignment Scores:  
Pred. No.: 0.153 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9

US-09-705-500a-1 (1-503) x US-09-365-705-1 (1-144)

QY 142 CTGCAAGTATTCGGGGGCTGACCTAGACCACTTGCATGATTCCTCTTGATTTG 201  
|||:|||||  
Db 34 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 47  
|||:|||||  
QY 202 -----CTGCACCTTGAACATTTTGTGCCAT---TATATTGCATTAGATTTA 249  
|||:|||||  
Db 48 LeuAsnProLeuValLeuProGluTyrLeuIleHisAlaPheMetCysValMetPheLeu 67  
|||:|||||  
QY 250 TAATTAAATGATATTAGTTTGGCTGAGTACTGCAATAAAC-----AGT 297  
|||:|||||  
Db 68 -----CysAlaIleAlaGluTyrPheuThrLeuGlyLeuAsnMetProLeuLeuAla 83  
|||:|||||  
QY 298 GAGCATATCTGG---TATATGTCA----- 318  
|||:|||||  
Db 84 TyrHisIleTyrArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103  
|||:|||||  
QY 319 TTATTATGTTAAATTACATTTTAAAGCTCCATGTCATATAAAGTTATGAACATAT 378  
|||:|||||  
Db 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGluGlyTyr----- 120  
|||:|||||  
QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420  
|||:|||||  
Db 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130  
|||:|||||

RESULT 3  
US-09-702-705-327  
Sequence 327, Application US/09702705  
Patent No. 6504010  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodges, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedrick, Tom  
APPLICANT: Carter, Darick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
TITLE REFERENCE: 210121.478C14  
CURRENT APPLICATION NUMBER: US/09/702,705



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; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-702-705-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACCAAGTTTGATGATCTCTCTTGATTTG 201
Db 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
QY 250 TAAATTAAATGATATTAGTTTGTGCTGAGTACGATCAATAAC-----AGT 297
Db 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTCATATAAGGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnAlaAspIleuAlaTyrCysGlnYsgIuGlyTyrP----- 120
QY 379 CATGTAATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db 121 -----CysYsLeuAlaPheTyrLeuAlaPhe 130

RESULT 4
US-09-736-457-327
; Sequence 327, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-702-705-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACCAAGTTTGATGATCTCTCTTGATTTG 201
Db 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
QY 250 TAAATTAAATGATATTAGTTTGTGCTGAGTACGATCAATAAC-----AGT 297
Db 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTCATATAAGGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnAlaAspIleuAlaTyrCysGlnYsgIuGlyTyrP----- 120
QY 379 CATGTAATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db 121 -----CysYsLeuAlaPheTyrLeuAlaPhe 130

RESULT 5
US-09-614-124B-327
; Sequence 327, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-614-124B-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACCAAGTTTGATGATCTCTCTTGATTTG 201
Db 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
QY 250 TAAATTAAATGATATTAGTTTGTGCTGAGTACGATCAATAAC-----AGT 297
Db 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTCATATAAGGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnAlaAspIleuAlaTyrCysGlnYsgIuGlyTyrP----- 120
QY 379 CATGTAATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db 121 -----CysYsLeuAlaPheTyrLeuAlaPhe 130
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Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-736-457-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACCAAGTTTGATGATCTCTCTTGATTTG 201
Db 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
QY 250 TAAATTAAATGATATTAGTTTGTGCTGAGTACGATCAATAAC-----AGT 297
Db 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTCATATAAGGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnAlaAspIleuAlaTyrCysGlnYsgIuGlyTyrP----- 120
QY 379 CATGTAATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db 121 -----CysYsLeuAlaPheTyrLeuAlaPhe 130

RESULT 5
US-09-614-124B-327
; Sequence 327, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-614-124B-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACCAAGTTTGATGATCTCTCTTGATTTG 201
Db 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
QY 250 TAAATTAAATGATATTAGTTTGTGCTGAGTACGATCAATAAC-----AGT 297
Db 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTCATATAAGGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnAlaAspIleuAlaTyrCysGlnYsgIuGlyTyrP----- 120
QY 379 CATGTAATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db 121 -----CysYsLeuAlaPheTyrLeuAlaPhe 130
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Db 48 LeuAnpProLeuValLeuPProGluTyrLeuIleHisAlaPhePheCysValMetPheLeu 67
QY 250 TAAATTTAAATGATTTAGCTTTTGCGCTGAGTACTGCAATTAAC-----AGT 297
Db 68 -----CysAlaAlaGluTrpLeuThrLeuGlyLeuAsnMetProLeuLeuAla 83
QY 298 GAGCATATCTGG---TATATGTCA----- 318
Db 84 TyrHisIleTrpArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTTATTTGTTAAATTTACATTTTAACTCCATGTGCATTAATGAAGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGlnLysGlnLysTrp----- 120
QY 379 CATGGTAATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420
Db 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130

RESULT 6
US-09-671-325-327
; Sequence 327, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Manion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-671-325-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-671-325-327 (1-144)
QY 142 CTCGAGAGTGAATTCGGGGCTGACCTAGACCACTTGCAATGATTCCTCTTGATTTG 201
Db 34 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----CTGCACCTTTAGACATTTTGTGCCAT---TATATTTGCATTAATGAATTA 249
Db 48 LeuAsnProLeuValLeuPProGluTyrLeuIleHisAlaPhePheCysValMetPheLeu 67
QY 250 TAAATTTAAATGATTTAGCTTTTGCGCTGAGTACTGCAATTAAC-----AGT 297
Db 68 -----CysAlaAlaGluTrpLeuThrLeuGlyLeuAsnMetProLeuLeuAla 83
QY 298 GAGCATATCTGG---TATATGTCA----- 318
Db 84 TyrHisIleTrpArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTTATTTGTTAAATTTACATTTTAACTCCATGTGCATTAATGAAGTTATGAACATAT 378
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Db 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGlnLysGlnLysTrp----- 120
QY 379 CATGGTAATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420
Db 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130

RESULT 7
US-09-589-184-327
; Sequence 327, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Manion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C08
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-184-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-589-184-327 (1-144)
QY 142 CTCGAGAGTGAATTCGGGGCTGACCTAGACCACTTGCAATGATTCCTCTTGATTTG 201
Db 34 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----CTGCACCTTTAGACATTTTGTGCCAT---TATATTTGCATTAATGAATTA 249
Db 48 LeuAsnProLeuValLeuPProGluTyrLeuIleHisAlaPhePheCysValMetPheLeu 67
QY 250 TAAATTTAAATGATTTAGCTTTTGCGCTGAGTACTGCAATTAAC-----AGT 297
Db 68 -----CysAlaAlaGluTrpLeuThrLeuGlyLeuAsnMetProLeuLeuAla 83
QY 298 GAGCATATCTGG---TATATGTCA----- 318
Db 84 TyrHisIleTrpArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTTATTTGTTAAATTTACATTTTAACTCCATGTGCATTAATGAAGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGlnLysGlnLysTrp----- 120
QY 379 CATGGTAATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420
Db 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130

RESULT 8
US-09-658-824-327
; Sequence 327, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
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APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Pan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.478C11  
CURRENT APPLICATION NUMBER: US/09/658,824  
CURRENT FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 1788  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 327  
LENGTH: 144  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-658-824-327

Alignment Scores:  
Pred. No.: 0.153 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9

US-09-705-500a-1 (1-503) x US-09-658-824-327 (1-144)

QY 142 CTGCAGAGTATTGGGGGCTGACCTAGACCACTTGATCTCTCTTGATTTG 201  
|||:|||||  
Db 34 LeuylsThraBpYrlysaBnProilLeaspGln-----CysaBnThr 47  
QY 202 -----GTGCACCTTAGACATTTTGTGCCAT--TATATTGCATTATGATTTA 249  
|||:|||||  
Db 48 LeuBnProleuValleuProgluYrleuIlehisAlaBneBheCysValMetPheleu 67  
QY 250 TAAATTAATGATATTAGTTTGGCTGAGTACTGATGAATAAAC-----AGT 297  
|||:|||||  
Db 68 -----CysAlaAlaGluTrpLeuThrleuGlyLeuBnMetProleuLeuAla 83  
QY 298 GAGCATATCTGG--TATATGTCA----- 318  
|||:|||||  
Db 84 TyhisIleTrpArgIyMetSerArgProValMetSerGlyProgluYleuYrAspPro 103  
QY 319 TTATTATTGTAAATTACATTTTAACTCATGTGCATATTAAGTTATGAACATAT 378  
|||:|||||  
Db 104 ThrThrIleMetAsnAlaAspIleleuAlaIyrcCysGlnlysgInduIyTrp----- 120  
QY 379 CATGGTAATGACAGATGCAAGTTA--TTTATTGGCTTATTTT 420  
|||:|||||  
Db 121 -----CysLysLeuAlaBheYrleuLeuAlaPhe 130

RESULT 9

US-09-257-179-63  
Sequence 63, Application US/09257179  
Patent No. 6410709  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 29 Human Secreted Proteins  
FILE REFERENCE: P2015P1  
CURRENT APPLICATION NUMBER: US/09/257,179  
CURRENT FILING DATE: 1998-02-25  
EARLIER APPLICATION NUMBER: PCT/US98/17709  
EARLIER FILING DATE: 1998-08-27  
EARLIER APPLICATION NUMBER: 60/056,270  
EARLIER FILING DATE: 1997-08-29  
EARLIER APPLICATION NUMBER: 60/056,271  
EARLIER FILING DATE: 1997-08-29  
EARLIER APPLICATION NUMBER: 60/056,247  
EARLIER FILING DATE: 1997-08-29

EARLIER APPLICATION NUMBER: 60/056,073  
EARLIER FILING DATE: 1997-08-29  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 63  
LENGTH: 145  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (145)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-257-179-63

Alignment Scores:  
Pred. No.: 0.153 Length: 145  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9

US-09-705-500a-1 (1-503) x US-09-257-179-63 (1-145)

QY 142 CTGCAGAGTATTGGGGGCTGACCTAGACCACTTGATCTCTCTTGATTTG 201  
|||:|||||  
Db 34 LeuylsThraBpYrlysaBnProilLeaspGln-----CysaBnThr 47  
QY 202 -----GTGCACCTTAGACATTTTGTGCCAT--TATATTGCATTATGATTTA 249  
|||:|||||  
Db 48 LeuBnProleuValleuProgluYrleuIlehisAlaBneBheCysValMetPheleu 67  
QY 250 TAAATTAATGATATTAGTTTGGCTGAGTACTGATGAATAAAC-----AGT 297  
|||:|||||  
Db 68 -----CysAlaAlaGluTrpLeuThrleuGlyLeuBnMetProleuLeuAla 83  
QY 298 GAGCATATCTGG--TATATGTCA----- 318  
|||:|||||  
Db 84 TyhisIleTrpArgIyMetSerArgProValMetSerGlyProgluYleuYrAspPro 103  
QY 319 TTATTATTGTAAATTACATTTTAACTCATGTGCATATTAAGTTATGAACATAT 378  
|||:|||||  
Db 104 ThrThrIleMetAsnAlaAspIleleuAlaIyrcCysGlnlysgInduIyTrp----- 120  
QY 379 CATGGTAATGACAGATGCAAGTTA--TTTATTGGCTTATTTT 420  
|||:|||||  
Db 121 -----CysLysLeuAlaBheYrleuLeuAlaPhe 130

RESULT 10

US-09-823-038A-48  
Sequence 48, Application US/09823038A  
Patent No. 6797271  
GENERAL INFORMATION:  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevin  
APPLICANT: Onrust, Rene  
APPLICANT: Kumble, Anand  
APPLICANT: Muirson, Greg  
TITLE OF INVENTION: Compositions isolated from Stromal Cells  
FILE REFERENCE: 11000.1037C3  
CURRENT APPLICATION NUMBER: US/09/823,038A  
CURRENT FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 48  
LENGTH: 664  
TYPE: PRT  
ORGANISM: Mouse  
US-09-823-038A-48

Alignment Scores:

Pred. No.:	0.293	Length:	664
Score:	74.50	Matches:	39
Percent Similarity:	45.89%	Conservative:	28
Best Local Similarity:	26.71%	Mismatches:	53
Query Match:	8.52%	Indels:	26
DB:	4	Gaps:	8

OY		3	ATATATTATCTCAACAAATACATAATATCTCAACATACAGAAAGAAGCATTCCTCAACAATTT	62
Dd		24	IIeTfclglyserlrrh-PheLeutylrleuLysPheLeuValValITrpAlalaLeuValIeuLe	43
OY		63	GCTAGTTTTTGC-----TTCTCTTTGCCCCACCCTACTCCCTCCAATTCCTCCTTA	118
Dd		43	uLaaspPheValIeuGluUpheArgPheGlnTyrlLeutTrpPro-----	57
OY		117	CTTCCAAAGTGTCGTCTTGCTTGGCTGAGAGTATTCGGGGCGCTGCATGACCGATT	176
Dd		58	-PheTrpPhePharileArgSerValIyAspSerPheArgTyrgInslgLyse--Alaph	76
OY		177	TGCATGATCTCTCTCTGTCGATTTGGTGCACCTTAGAACATTTTGTGCCATTAATTTT	238
Dd		76	eSerValPhePheValCys-----ValAla-----PheThrSerAmnIlleIcy	91
OY		237	CATTATGCTATTTTAATTAAATGAATATTAGCTTTTGGCTGAGTACTGCMAATPAACAG	296
Dd		91	sLeuLeuPheIleProIleGln---TriPhePhePheAlaAlaSerTrlTyValITrpVa	110
OY		297	TGAGCAATCTGGTAT-----ATGTCATATTATTATGT	328
Dd		110	IgIntlyValITriPheIsThrgLArgClvalYcysLeuProthrValasrLeuITrple	130
OY		330	TAAATTACATTTTAAAGCTCCATGTCAGATATPAAGGTTATGAAACATATCATGTGAATGA	388
Dd		130	uPheValTyrlleGlualAlalaIleArgPheLysAspLeuLysAsnPheHis---Valas	149
OY		390	CAGATGCAAGTATTT	405
Dd		149	pLeuCysArgProphe	154

```

RESULT 11
US-09-270-767-46166
; Sequence 46166, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCES: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46166
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46166

```

Alignment Scores:	
Pred. No.:	0.443
Score:	72.50
Percent Similarity:	39.02%
Best Local Similarity:	26.22%
Query Match:	8.20%
DB:	4
Length:	333
Matches:	43
Conservative:	21
Mismatches:	53
Indels:	8
Gaps:	47

US-09-705-500A-1 (1-503) X US-09-270-767-46166 (1-330)

397 TGCATCTGTCATTACCATGATATGTTTCATAAC---CTTATATGCACATGAGCTTAAA 341

```

Db      86  Cys11LeuVal19AlaSer15HisSer17IleCysMetHis15IlePro1Le--- 104
Qy      340 AAATGTAATTTCACAAATTAATATGACATATACAGAGTATGCTCAGCTGTTATTCAGATAC 281
Db      105 -----***PheThrIserAsnArg--IleGlnCysLeu11MetAsn 117
Qy      280 TCAGCCAAACACCTTAATATATCATTTTAATTTAATAATACATATAGCAATATTAATGGACA 221
Db      118 ArgAla1LeuGln1AsnSer1Le-----Thr1Asn***AsnGly1LeuVal 132
Qy      220 AAAATGTCTTAAGTCGACACCAATATACACAGAGAAAGATCATAGCAACTGGTCTTAAGTCAG 161
Db      132 s1ysGlnAsnSerAsn1ysGln1Thr1Thr1Gln1ysAsn1ysGln1LeuArg1LeuAs 152
Qy      160 CCCCAGATATCATCTTCGCGACGAACAC-----AAGACGAAGCTTTGGAAGTTTAAGGGGG 107
Db      152 nAsn1ys1ys1ys1e1r1Ie1ys1Sh1e1rGln1y1s1e1ys1Gln1y1s1e1ys1e1ys1 172
Qy      106 AATTGAGAGCA-----GTAGGCTGGGGGAAAGACAGACAAAAA 68
Db      172 1yCysGly1yGln1u1r1Thr1y1sGln1SerGln1LeuArg1TrpGly1ys1e1**Asn1ys 192
Qy      67 CTAGCAACATTTGAGGAATGCTCT----- 45
Db      192 e1serAsn1ys1e1r1ys1Thr1Ser1ys1****Leu****Arg1y1s1y1s1e1ys1e1ys1 212
Qy      44 -----TCCTTCTGATATGTGA------TATATGATTTGA 14
Db      212 hr1e1p1Arg1ys1Thr1Ala1ys1***PheCys11e1Val1Arg1Arg1Asn1y1s1y1e1ys1 232
Qy      13  GATACATA 6
Db      232 eut1y1r1e1u 234

```

```

RESULT 12
US-09-270-767-34960
; Sequence 34960, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7336-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34960
; LENGTH: 353
; TYPE: PR1
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34960

```

Alignment scores:	
Pred. No.:	0.622
Score:	71.50
Percent Similarity:	40.00%
Best Local Similarity:	25.52%
Query Match:	8.18%
DB:	4
	7
Length:	35
Matches:	27
Conservative:	31
Mismatches:	50
Indels:	37
Gaps:	7

US-09-705-500A-1 (1-503) X US-09-270-767-34960 (1-353)

[illegible]

```

Db      266 ThrProIleSerPheValCysValThrLeuCysTrpLeu-----SerAlaGln 281
Qy      166 CTAGACCAAGTTTGCATGATTCCTCTCTGTGATTGGTTGCACCTTAGACATTTTGTGC 225
Db      282 LeuAspLeuThrAlaIlePheLeuSerValIleVal----- 294
Qy      226 CATTAATTTGCTATGATTTATATAATTAATGATTTAGTTTGGCTGAGTACT 285
Db      295 PhePheValIleuIlePhePheArgAspPheAsnGluPhe-----PhePheAlaValVal 312
Qy      286 GGAATTAACAGTGCATATCTGTATATGTCATTTATTTATTTGTTAAATTGATTTTAA 345
Db      313 LeuValSerSerGlnIlys**TyrTyr-----LeuPhePheValIleuLeuPhePhe--- 329
Qy      346 GCTCCATGTGCATATTAAGGTTATGAAACATATCATGATGATGACAGATGCAAGTTATT 405
Db      330 -----CysPheSerPhe 333
Qy      406 TATTGCTTATTTT 420
Db      334 LeuValPheIlePhe 338

RESULT 13
US-09-270-767-50177
; Sequence 50177, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50177
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50177

```

```

Alignment Scores:
Pred. No.: 0.622 Length: 353
Score: 71.50 Matches: 37
Percent Similarity: 40.00% Conservative: 21
Best Local Similarity: 25.52% Mismatches: 50
Query Match: 8.18% Indels: 37
DB: 4 Gaps: 7

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US-09-705-500a-1 (1-503) x US-09-270-767-50177 (1-353)

```

Qy      1 CTATATATGATCTACATACATATATCTACATACAGAAAGACAGTTCTCACATG 60
Db      226 LeuLeuProTyrTyrValPheIleHisValTyrIleHisProIleuAsnIleLeuThrAsn 245
Qy      61 TTG-----CTAGTTTTCCTCTCTTTCCTCCCAACCTTACCTCCCTTCAT----- 105
Db      246 LeuTyrTyrLeuLeuCysAlaSerThrSerSerSerSerProIleAsn**ProIle 265
Qy      106 TCCCCCTTAACCTCCAAAGCTTGTCTGTGTTGTGAGAGTGATGGGGGCTGAC 165
Db      266 ThrProIleSerPheValCysValThrLeuCysTrpLeu-----SerAlaGln 281
Qy      166 CTAGACCAAGTTTGCATGATTCCTCTCTGTGATTGGTTGCACCTTAGACATTTTGTGC 225
Db      282 LeuAspLeuThrAlaIlePheLeuSerValIleVal----- 294
Qy      226 CATTAATTTGCTATGATTTATATAATTAATGATTTAGTTTGGCTGAGTACT 285
Db      295 PhePheValIleuIlePhePheArgAspPheAsnGluPhe-----PhePheAlaValVal 312

```

```

Qy      286 GGAATTAACAGTGCATATCTGTATATGTCATTTATTTATTTGTTAAATTGATTTTAA 345
Db      313 LeuValSerSerGlnIlys**TyrTyr-----LeuPhePheValIleuLeuPhePhe--- 329
Qy      346 GCTCCATGTGCATATTAAGGTTATGAAACATATCATGATGATGACAGATGCAAGTTATT 405
Db      330 -----CysPheSerPhe 333
Qy      406 TATTGCTTATTTT 420
Db      334 LeuValPheIlePhe 338

RESULT 14
US-09-248-796A-27951
; Sequence 27951, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27951
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27951

```

```

Alignment Scores:
Pred. No.: 0.493 Length: 63
Score: 70.50 Matches: 17
Percent Similarity: 52.94% Conservative: 10
Best Local Similarity: 33.33% Mismatches: 19
Query Match: 8.07% Indels: 5
DB: 4 Gaps: 2

```

US-09-705-500a-1 (1-503) x US-09-248-796A-27951 (1-63)

```

Qy      19 TACATATATCTACACATACAG-----AAAGACAGTTCTCACATGTTG--- 63
Db      8 TyrIleLeuLeuTyrIleIleValIleProIleProIleAsnIleAlaThrAlaSerIleuHis 27
Qy      64 CTAGTTTTCCTCTCTTTCCTCCCAACCTTACCTCCCTTAACTTCCAA 123
Db      28 SerValPheCysPheThrTyrSerHisAsnIleProIleAsnSerProIleHisAspHis 47
Qy      124 AGCTTGTCTGTGTGTTGCTGCGAGAGTATTCG 156
Db      48 AspPheGluValIlePhePheSerThrGlySer 58

RESULT 15
US-09-134-000C-5472
; Sequence 5472, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5472
; LENGTH: 405

```

TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-5472

## Alignment Scores:

Pred. No.:	0.895	Length:	405
Score:	70.50	Matches:	31
Percent Similarity:	40.68%	Conservative:	17
Best Local Similarity:	26.27%	Mismatches:	46
Query Match:	8.07%	Indels:	24
DB:	4	Gaps:	4

US-09-705-500a-1 (1-503) x US-09-134-000C-5472 (1-405)

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QY 79 TCCTTCCCGACCCCTACTCCCTCCCAATTCCTTAACTTCCAAAGCTTGCTGTGT 138
   |||
Db 7 AsnPhcProHisMetIleProIlyrAsnAlaProIlyrPheValLeuLeuIleAla 26
QY 139 TTGCTGCAGAGTAGATTGGGGGCTGACCTAGACCAAGTTGCATGATTTCTCTGTGAT 198
   |||
Db 27 LeuLeuPro-MetIleLeuThrLeuAlaIleIySGlyThrArg----- 40
QY 199 TTGCTGCACCTTAGACATTTTGTGCCATTATTTGCATTTATGATTTTATATTAA 258
   |||
Db 41 -TTPProIlyrGlnThrLeuValThrLeuValPheLeu-TyrIle----- 55
QY 259 TGAATTATTAGGTTTTGGCTGACTGCAATAAACAAGGACATCTGGTATATGCA 318
   |||
Db 56 -----SerPheGlyGlyGlnPheTrpGlnGlnGlyValAlaLeuIleValIyValI 73
QY 319 TTATTTATTTGTTAAATTACATTTTAAAGCTCCATGTCATATATAAGTTATGAAACATAT 378
   |||
Db 73 Ie-TyrGlnThrLeuLeuThrTp-----GlyTyrAlaIaIy 85
QY 379 CATGTTATGACAGATGCAAG--TTATTTTATTTGCTTATTTTATA 423
   |||
Db 86 ArgLysAsnLysAsnAlaGlyTTPValPheTyrLeuAlaValPheLeu 101
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Search completed: November 22, 2004, 17:50:03  
Job time : 24.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 22, 2004, 17:42:57 ; Search time 271.5 Seconds  
(without alignments)

1312.163 Million cell updates/sec

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Perfect score: 874  
Sequence: 1 ccatatgctctacacaa.....taataaagtgctgcttta 503

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 3141230

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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-LONGLOG -DEV TIMEOUT=120 -WARN=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA: \*  
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2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	78.5	9.0	291	14	US-10-017-161-2388	Sequence 2388, App
2	78.5	9.0	291	14	US-10-292-798-2030	Sequence 2030, App
3	78	8.9	338	14	US-10-017-161-2058	Sequence 2058, App
4	78	8.9	338	14	US-10-292-798-1704	Sequence 1704, App
5	75.5	8.6	298	14	US-10-017-161-2194	Sequence 2194, App
6	75.5	8.6	298	14	US-10-292-798-1840	Sequence 1840, App
7	75.5	8.5	471	15	US-10-108-2604-4551	Sequence 4551, App
8	75	8.6	109	15	US-10-424-599-189266	Sequence 189266, App
9	75	8.6	142	9	US-09-765-205-2	Sequence 2, App1
10	75	8.6	144	9	US-09-978-295A-322	Sequence 322, App
11	75	8.6	144	9	US-09-736-457-327	Sequence 327, App
12	75	8.6	144	9	US-09-978-657-322	Sequence 322, App
13	75	8.6	144	9	US-09-902-941-327	Sequence 327, App
14	75	8.6	144	9	US-09-978-182A-322	Sequence 322, App
15	75	8.6	144	9	US-09-999-832A-322	Sequence 322, App
16	75	8.6	144	9	US-09-849-626-327	Sequence 327, App
17	75	8.6	144	10	US-09-978-189-322	Sequence 322, App
18	75	8.6	144	10	US-09-978-608A-322	Sequence 322, App
19	75	8.6	144	10	US-09-978-585A-322	Sequence 322, App
20	75	8.6	144	10	US-09-978-191A-322	Sequence 322, App
21	75	8.6	144	10	US-09-978-403A-322	Sequence 322, App
22	75	8.6	144	10	US-09-978-564A-322	Sequence 322, App
23	75	8.6	144	10	US-09-999-833A-322	Sequence 322, App
24	75	8.6	144	10	US-09-981-915A-322	Sequence 322, App
25	75	8.6	144	10	US-09-978-824-322	Sequence 322, App
26	75	8.6	144	10	US-09-918-585A-322	Sequence 322, App
27	75	8.6	144	10	US-09-999-834A-322	Sequence 322, App
28	75	8.6	144	10	US-09-978-423A-322	Sequence 322, App
29	75	8.6	144	10	US-09-978-193A-322	Sequence 322, App
30	75	8.6	144	10	US-09-999-830A-322	Sequence 322, App
31	75	8.6	144	10	US-09-978-757A-322	Sequence 322, App
32	75	8.6	144	10	US-09-978-187B-322	Sequence 322, App
33	75	8.6	144	10	US-09-978-643A-322	Sequence 322, App
34	75	8.6	144	10	US-09-476-300-327	Sequence 327, App
35	75	8.6	144	10	US-09-978-755A-322	Sequence 322, App
36	75	8.6	144	10	US-09-978-188A-322	Sequence 322, App
37	75	8.6	144	10	US-09-978-188A-322	Sequence 322, App
38	75	8.6	144	10	US-09-978-681A-322	Sequence 322, App
39	75	8.6	144	10	US-09-978-194A-322	Sequence 322, App
40	75	8.6	144	10	US-09-999-829A-322	Sequence 322, App
41	75	8.6	144	10	US-09-978-299A-322	Sequence 322, App
42	75	8.6	144	10	US-09-978-544A-322	Sequence 322, App
43	75	8.6	144	10	US-09-978-665A-322	Sequence 322, App
44	75	8.6	144	10	US-09-978-802A-322	Sequence 322, App
45	75	8.6	144	11	US-09-999-831A-322	Sequence 322, App

#### ALIGNMENTS

RESULT 1  
US-10-017-161-2388  
; Sequence 2388, Application US/10017161  
; Publication No. US20030143668A1  
GENERAL INFORMATION:  
; APPLICANT: SUMA, MAKIYO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2388  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-2388





QY 62 TGCTAGTTTTGCTTCTCTTTCCACCACCTACTCCCTCCAAATGCCCTTAAACTTCC 121  
DB 238 ----- 238  
QY 122 AAAGCTTCGTTGCTTGTCTGTCGACAGATGATTCGGGGGCTGACCTAGACCAAGTTGCAT 181  
DB 239 -----MetCysValCysAlaIyTrThrHisThrIleTyThrLeuCysValTyR 255  
QY 239 -----MetCysValCysAlaIyTrThrHisThrIleTyThrLeuCysValTyR 255  
DB 182 GATTCT-----TCTCTTGATTTGGTTGCAC 208  
QY 256 ThnHisTyThrHisTyValTyThrHisThrIleTyThrLeuCysValTyRHis 275  
DB 209 TTTAGACATTT--TGTCGC--ATTATATTGCATTAATGATTAATTAATGAT 262  
DB 276 TyArgHisTyValCysThrHisThrIleTyThrLeuCysValTyR----- 291  
QY 263 ATTAGGTTTTGGCTGAGTACGATGAATAACGATGACATCTGCTATA--TGTCAT 319  
DB 292 -----ThnHisThrIleTyThrLeuTyThrHis 301  
QY 320 TATTATGTGAATTACATTTTAACTCCATGTCATATAAAGTTATGAACATATC 379  
DB 302 ThrIleTyThrLeuTyRile-----LeuHisIleTyRileValTyRMeTyRile 319  
QY 380 ATCGTAATGACAGATGCAAGTTATTTATTTGCTTATTTTA 421  
DB 320 CysValTyThrHisAsnValTyRilePheThrSerPheMet 333  
RESULT 4  
US-10-292-798-1704  
; Sequence 1704, Application US/10292798  
; Publication No. US2003025833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: AUBURANT, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1704  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-798-1704  
Alignment Scores:  
Pred. No.: 1.77 Length: 338  
Score: 78.00 Matches: 32  
Percent Similarity: 33.12% Conservative: 41  
Best Local Similarity: 20.78% Mismatches: 62  
Query Match: 8.92% Indels: 7  
DB: 14 Gaps: 7  
US-09-705-500A-1 (1-503) x US-10-292-798-1704 (1-338)  
QY 2 TATATGTGATCTACATACATATATCTACACATAGAGAAGAAGAGATTCTACATGT 61  
DB 228 TyValCysValTyThrHisThrIleTyR----- 238  
QY 62 TGCTAGTTTTGCTTCTCTTTCCACCACCTACTCCCTCCAAATGCCCTTAAACTTCC 121  
DB 238 ----- 238  
QY 122 AAAGCTTCGTTGCTTGTCTGTCGACAGATGATTCGGGGGCTGACCTAGACCAAGTTGCAT 181

DB 239 -----MetCysValCysAlaIyTrThrHisThrIleTyThrLeuCysValTyR 255  
QY 182 GATTCT-----TCTCTTGATTTGGTTGCAC 208  
DB 256 ThnHisTyThrHisTyValTyThrHisThrIleTyThrLeuCysValTyRHis 275  
QY 209 TTTAGACATTT--TGTCGC--ATTATATTGCATTAATGATTAATTAATGAT 262  
DB 276 TyArgHisTyValCysThrHisThrIleTyThrLeuCysValTyR----- 291  
QY 263 ATTAGGTTTTGGCTGAGTACGATGAATAACGATGACATCTGCTATA--TGTCAT 319  
DB 292 -----ThnHisThrIleTyThrLeuTyThrHis 301  
QY 320 TATTATGTGAATTACATTTTAACTCCATGTCATATAAAGTTATGAACATATC 379  
DB 302 ThrIleTyThrLeuTyRile-----LeuHisIleTyRileValTyRMeTyRile 319  
QY 380 ATCGTAATGACAGATGCAAGTTATTTATTTGCTTATTTTA 421  
DB 320 CysValTyThrHisAsnValTyRilePheThrSerPheMet 333  
RESULT 5  
US-10-017-161-2194  
; Sequence 2194, Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: AUBURANT, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; PRIOR FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2194  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-2194  
Alignment Scores:  
Pred. No.: 3.58 Length: 298  
Score: 75.50 Matches: 36  
Percent Similarity: 36.84% Conservative: 20  
Best Local Similarity: 23.68% Mismatches: 37  
Query Match: 8.64% Indels: 59  
DB: 14 Gaps: 6  
US-09-705-500A-1 (1-503) x US-10-017-161-2194 (1-298)  
QY 49 GTTCTCAATAGTTGCTAGTTTGTCTCTTTCCACCACCTACTCCCTCCAAATTC 108  
DB 74 ValLeuSerCysPheProValPheLeuSerPhe----- 85  
QY 109 CCCTTAACTTCCAAAGCTTGCTTGTGTTGCTGACAGATGATTCGGGGGCTGACCTA 166  
DB 86 -----PheLeuSerPheLeuSerCysLeuLeu----- 94  
QY 169 GACCAATTGATGATCTTCTCTTGATTTGGTTGCATTTAGACATTTTGGCAT 228  
DB 95 -----SerCysLeuLeuAlaCysPheArgAlaPheLeuLeuSer 107  
QY 229 TATATGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 276  
DB 108 -----CysPheLeuPheLeuSerPhe-----PheLeuSerPheTyRysPhePheLeu 123  
QY 277 -----CTGAGTACTGCAATTAACAGTATGACATATCTGATATATG 315



LENGTH: 109  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_141923C.1.pap  
US-10-424-599-189266

Alignment Scores:  
Pred. No.: 3.51 Length: 109  
Score: 75.00 Matches: 24  
Percent Similarity: 42.53% Conservative: 13  
Best Local Similarity: 27.59% Mismatches: 36  
Query Match: 8.58% Indels: 14  
DB: 15 Gaps: 2

US-09-705-500a-1 (1-503) x US-10-424-599-189266 (1-109)

QY 73 TGCTTCTCTTC-----CCGACCTACTCCC 99  
Db 10 CysAlaSerPheAsnSerLeuHisIlyMetGlyTyrValSerGlnHisLeuProPro 29  
QY 100 TCCAAATTCCTTAACTTCCAAAGCTTC-----GTCTTGTTGCTGACAGT 150  
Db 30 ThrPheSerProLeuHisPheSerValPheThrPheSerIleYrThrLeuHisHis 49  
QY 151 GATTCGGGGGCTGACCTAGACAGTTTGTCATGATTCCTCTGCTTGATTTGGTGCATT 210  
Db 50 HisValValPheAspIleThrGlnPheSerLeuValPheSerCysLeuAlaLeuSerLeu 69  
QY 211 TAGACATTTTGGCCATTATATTGTCATTATATTAAATGATTTAGT 270  
Db 70 CysPheProPheValCysLeuTyrrPhePheGlnLeuPheHisSerLeuPheSerAlaLeuGln 89  
QY 271 TTTTGCTGAGTACTGGAATA 291  
Db 90 ValTrpAsnGlnThrAsnLeu 96

RESULT 9  
US-09-765-205-2  
Sequence 2, Application US/09765205  
Patent No. US20020034800A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Li  
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
FILE REFERENCE: 1458, 004/200130, 449  
CURRENT APPLICATION NUMBER: US/09/765, 205  
CURRENT FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US/09/212, 440  
PRIOR FILING DATE: 1998-12-16  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 142  
TYPE: PRT  
ORGANISM: human  
US-09-765-205-2

Alignment Scores:  
Pred. No.: 3.67 Length: 142  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
DB: 9 Gaps: 9

US-09-705-500a-1 (1-503) x US-09-765-205-2 (1-142)

QY 142 CTGCAGAGTATTCGGGGGCTGACCTAGACAGTTTGATGATTTCTTCTGTGATTTG 201  
Db 32 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 45  
QY 202 -----GTTCACCTTTAGACATTTTGTGCCAT--TATATTGCATTATGATTTA 249

Db 46 LeuAsnProLeuValLeuProGlnTyrLeuIleHisAlaPhePheCysValMetPheLeu 65  
QY 250 TAATTTAATGATATTTAGTTTGGCTGAGTACTGGAATTAAC-----AGT 297  
Db 66 -----CysAlaAlaGlnTyrPheThrLeuGlyLeuAsnMetProLeuAla 81  
QY 298 GAGCATATCTGG--TATATGTCA----- 318  
Db 82 TyrHisIleTrpAspGlyTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 101  
QY 319 TTATTTATGTTAATTAATTTTAAAGCTCCATGTCATTAAGGTTATGAACAATAT 378  
Db 102 ThrThrIleLeuAsnAlaAspIleLeuAlaTyrCysGlnLysGlnGlyTrp----- 118  
QY 379 CATGGTAATGACAGATGCAAGTTA--TTTATTTGCTTATTTT 420  
Db 119 -----CysLeuLeuAlaPheTyrLeuLeuAlaPhe 128

RESULT 10  
US-09-978-295A-322  
Sequence 322, Application US/0978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fond, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978, 295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/074450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11

1	PRIOR APPLICATION NUMBER: 60/077791	1	PRIOR FILING DATE: 1998-04-22	1	PRIOR APPLICATION NUMBER: 60/082804	1	PRIOR FILING DATE: 1998-04-22
2	PRIOR FILING DATE: 1998-03-12	2	PRIOR APPLICATION NUMBER: 60/078004	2	PRIOR FILING DATE: 1998-04-22	2	PRIOR APPLICATION NUMBER: 60/082700
3	PRIOR FILING DATE: 1998-03-13	3	PRIOR APPLICATION NUMBER: 60/078886	3	PRIOR FILING DATE: 1998-04-22	3	PRIOR APPLICATION NUMBER: 60/082797
4	PRIOR FILING DATE: 1998-03-20	4	PRIOR APPLICATION NUMBER: 60/078936	4	PRIOR FILING DATE: 1998-04-22	4	PRIOR APPLICATION NUMBER: 60/082760
5	PRIOR FILING DATE: 1998-03-20	5	PRIOR APPLICATION NUMBER: 60/078910	5	PRIOR FILING DATE: 1998-04-23	5	PRIOR APPLICATION NUMBER: 60/083366
6	PRIOR APPLICATION NUMBER: 60/078939	6	PRIOR FILING DATE: 1998-03-20	6	PRIOR FILING DATE: 1998-04-27	6	PRIOR APPLICATION NUMBER: 60/083363
7	PRIOR FILING DATE: 1998-03-20	7	PRIOR APPLICATION NUMBER: 60/079294	7	PRIOR APPLICATION NUMBER: 60/083322	7	PRIOR APPLICATION NUMBER: 60/083428
8	PRIOR FILING DATE: 1998-03-25	8	PRIOR APPLICATION NUMBER: 60/079656	8	PRIOR FILING DATE: 1998-04-29	8	PRIOR APPLICATION NUMBER: 60/083322
9	PRIOR FILING DATE: 1998-03-26	9	PRIOR APPLICATION NUMBER: 60/079664	9	PRIOR FILING DATE: 1998-04-29	9	PRIOR APPLICATION NUMBER: 60/083499
10	PRIOR FILING DATE: 1998-03-27	10	PRIOR APPLICATION NUMBER: 60/079669	10	PRIOR FILING DATE: 1998-04-29	10	PRIOR APPLICATION NUMBER: 60/083454
11	PRIOR FILING DATE: 1998-03-27	11	PRIOR APPLICATION NUMBER: 60/079663	11	PRIOR FILING DATE: 1998-04-29	11	PRIOR APPLICATION NUMBER: 60/083555
12	PRIOR APPLICATION NUMBER: 60/079728	12	PRIOR FILING DATE: 1998-03-27	12	PRIOR FILING DATE: 1998-04-29	12	PRIOR APPLICATION NUMBER: 60/083554
13	PRIOR FILING DATE: 1998-03-27	13	PRIOR APPLICATION NUMBER: 60/079786	13	PRIOR FILING DATE: 1998-04-29	13	PRIOR APPLICATION NUMBER: 60/083558
14	PRIOR FILING DATE: 1998-03-27	14	PRIOR APPLICATION NUMBER: 60/079920	14	PRIOR FILING DATE: 1998-04-29	14	PRIOR APPLICATION NUMBER: 60/083555
15	PRIOR FILING DATE: 1998-03-30	15	PRIOR APPLICATION NUMBER: 60/079923	15	PRIOR FILING DATE: 1998-04-29	15	PRIOR APPLICATION NUMBER: 60/083500
16	PRIOR FILING DATE: 1998-03-30	16	PRIOR APPLICATION NUMBER: 60/080105	16	PRIOR FILING DATE: 1998-04-29	16	PRIOR APPLICATION NUMBER: 60/083742
17	PRIOR FILING DATE: 1998-03-31	17	PRIOR APPLICATION NUMBER: 60/080107	17	PRIOR FILING DATE: 1998-04-30	17	PRIOR APPLICATION NUMBER: 60/084366
18	PRIOR FILING DATE: 1998-03-31	18	PRIOR APPLICATION NUMBER: 60/080165	18	PRIOR FILING DATE: 1998-05-05	18	PRIOR APPLICATION NUMBER: 60/084414
19	PRIOR FILING DATE: 1998-03-31	19	PRIOR APPLICATION NUMBER: 60/080194	19	PRIOR FILING DATE: 1998-05-06	19	PRIOR APPLICATION NUMBER: 60/084414
20	PRIOR FILING DATE: 1998-03-31	20	PRIOR APPLICATION NUMBER: 60/080327	20	PRIOR FILING DATE: 1998-05-06	20	PRIOR APPLICATION NUMBER: 60/084639
21	PRIOR FILING DATE: 1998-04-01	21	PRIOR APPLICATION NUMBER: 60/080328	21	PRIOR FILING DATE: 1998-05-07	21	PRIOR APPLICATION NUMBER: 60/084627
22	PRIOR FILING DATE: 1998-04-01	22	PRIOR APPLICATION NUMBER: 60/080333	22	PRIOR FILING DATE: 1998-05-07	22	PRIOR APPLICATION NUMBER: 60/084644
23	PRIOR FILING DATE: 1998-04-01	23	PRIOR APPLICATION NUMBER: 60/080334	23	PRIOR FILING DATE: 1998-05-07	23	PRIOR APPLICATION NUMBER: 60/084599
24	PRIOR FILING DATE: 1998-04-01	24	PRIOR APPLICATION NUMBER: 60/081070	24	PRIOR FILING DATE: 1998-05-07	24	PRIOR APPLICATION NUMBER: 60/084600
25	PRIOR FILING DATE: 1998-04-08	25	PRIOR APPLICATION NUMBER: 60/081049	25	PRIOR FILING DATE: 1998-05-07	25	PRIOR APPLICATION NUMBER: 60/084627
26	PRIOR FILING DATE: 1998-04-08	26	PRIOR APPLICATION NUMBER: 60/081071	26	PRIOR FILING DATE: 1998-05-07	26	PRIOR APPLICATION NUMBER: 60/084644
27	PRIOR FILING DATE: 1998-04-08	27	PRIOR APPLICATION NUMBER: 60/081195	27	PRIOR FILING DATE: 1998-05-07	27	PRIOR APPLICATION NUMBER: 60/085333
28	PRIOR FILING DATE: 1998-04-08	28	PRIOR APPLICATION NUMBER: 60/081203	28	PRIOR FILING DATE: 1998-05-13	28	PRIOR APPLICATION NUMBER: 60/085338
29	PRIOR FILING DATE: 1998-04-09	29	PRIOR APPLICATION NUMBER: 60/081229	29	PRIOR FILING DATE: 1998-05-13	29	PRIOR APPLICATION NUMBER: 60/085322
30	PRIOR FILING DATE: 1998-04-09	30	PRIOR APPLICATION NUMBER: 60/081955	30	PRIOR FILING DATE: 1998-05-13	30	PRIOR APPLICATION NUMBER: 60/085588
31	PRIOR FILING DATE: 1998-04-15	31	PRIOR APPLICATION NUMBER: 60/081817	31	PRIOR FILING DATE: 1998-05-15	31	PRIOR APPLICATION NUMBER: 60/085700
32	PRIOR FILING DATE: 1998-04-15	32	PRIOR APPLICATION NUMBER: 60/081819	32	PRIOR FILING DATE: 1998-05-15	32	PRIOR APPLICATION NUMBER: 60/085688
33	PRIOR FILING DATE: 1998-04-15	33	PRIOR APPLICATION NUMBER: 60/081952	33	PRIOR FILING DATE: 1998-05-15	33	PRIOR APPLICATION NUMBER: 60/085579
34	PRIOR FILING DATE: 1998-04-15	34	PRIOR APPLICATION NUMBER: 60/081838	34	PRIOR FILING DATE: 1998-05-15	34	PRIOR APPLICATION NUMBER: 60/085580
35	PRIOR FILING DATE: 1998-04-15	35	PRIOR APPLICATION NUMBER: 60/082568	35	PRIOR FILING DATE: 1998-05-15	35	PRIOR APPLICATION NUMBER: 60/085572
36	PRIOR FILING DATE: 1998-04-21	36	PRIOR APPLICATION NUMBER: 60/082565	36	PRIOR FILING DATE		

PRIOR APPLICATION NUMBER: 60/085697

# Alignment Scores:

Score: 3.68 Length: 144  
 Percent Similarity: 75.00 Matches: 33  
 Best Local Similarity: 41.74% Conservative: 15  
 Query Match: 28.70% Mismatches: 27  
 DB: 9 Indels: 40  
 Gaps: 9

US-09-705-500a-1 (1-503) x US-09-978-295a-322 (1-144)

QY 142 CTGACAGGATTCGGGGGCTGACCTAGACGATTGATGATTTCTCTGTGATTG 201  
 DB 34 LeuysThraPgyrLyAsnProIleAspGln-----CysAsnThr 47  
 QY 202 -----GTTGACCTTTAGACATTTTGTGCAT---TATATTGCAATTATGATTTA 249  
 DB 48 LeuAsnProLeuValLeuProGlnuTyLeuIleHisAlaPhePheCysValMetPheLeu 67  
 QY 250 TAAATTAAATGATATTAGGTTTGGCTGAGTACTGGAATAAAC-----AGT 297  
 DB 68 -----CysAlaAlaGlnuTyPLeuThrLeuGlnLeuAsnMetProLeuLeuAla 83  
 QY 298 GAGCATATCTGG---TATATGTCA----- 318  
 DB 84 TyrHisIleTyrPArgTyMetSerArgProValMetSerGlyProGlyLeuTyAspPro 103  
 QY 319 TTATTATTGTTAAATTACATTTTAACTCCATGTGCATATAAGTTATGAACATAT 378  
 DB 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrcysGlnuysGlnuTyTrp----- 120  
 QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTGCTTATTTT 420  
 DB 121 -----CysLysLeuAlaPheTyrlleuLeuAlaPhe 130

## RESULT 11

US-09-736-457-327  
 Sequence 327, Application US/09736457  
 Patent No. US20020168637A1  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Tongtong  
 APPLICANT: Bangur, Chaitanya S.  
 APPLICANT: Iodes, Michael A.  
 APPLICANT: Fanger, Gary  
 APPLICANT: Vedvick, Tom  
 APPLICANT: Carter, Darrick  
 APPLICANT: Retter, Marc  
 APPLICANT: Mannion, Jane  
 APPLICANT: Fan, Liqun  
 APPLICANT: Wang, Liqun  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
 FILE REFERENCE: 210121.478C15  
 CURRENT APPLICATION NUMBER: US/09/736,457  
 CURRENT FILING DATE: 2000-12-13  
 NUMBER OF SEQ ID NOS: 1864  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 327  
 LENGTH: 144  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-736-457-327

# Alignment Scores:

Pred. No.: 3.68 Length: 144  
 Score: 75.00 Matches: 33  
 Percent Similarity: 41.74% Conservative: 15  
 Best Local Similarity: 28.70% Mismatches: 27  
 Query Match: 8.58% Indels: 40  
 DB: 9 Gaps: 9

US-09-705-500a-1 (1-503) x US-09-736-457-327 (1-144)

QY 142 CTGACAGGATTCGGGGGCTGACCTAGACGATTGATGATTTCTCTGTGATTG 201  
 DB 34 LeuysThraPgyrLyAsnProIleAspGln-----CysAsnThr 47  
 QY 202 -----GTTGACCTTTAGACATTTTGTGCAT---TATATTGCAATTATGATTTA 249  
 DB 48 LeuAsnProLeuValLeuProGlnuTyLeuIleHisAlaPhePheCysValMetPheLeu 67  
 QY 250 TAAATTAAATGATATTAGGTTTGGCTGAGTACTGGAATAAAC-----AGT 297  
 DB 68 -----CysAlaAlaGlnuTyPLeuThrLeuGlnLeuAsnMetProLeuLeuAla 83  
 QY 298 GAGCATATCTGG---TATATGTCA----- 318  
 DB 84 TyrHisIleTyrPArgTyMetSerArgProValMetSerGlyProGlyLeuTyAspPro 103  
 QY 319 TTATTATTGTTAAATTACATTTTAACTCCATGTGCATATAAGTTATGAACATAT 378  
 DB 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrcysGlnuysGlnuTyTrp----- 120  
 QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTGCTTATTTT 420  
 DB 121 -----CysLysLeuAlaPheTyrlleuLeuAlaPhe 130

## RESULT 12

US-09-978-697-322  
 Sequence 322, Application US/09978697  
 Patent No. US20020169284A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P26302P127  
 CURRENT APPLICATION NUMBER: US/09/978,697  
 CURRENT FILING DATE: 2001-10-16  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066364  
 PRIOR FILING DATE: 1997-11-21  
 PRIOR APPLICATION NUMBER: 60/077450



PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 3.68 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
DB: Gaps: 9

US-09-705-500A-1 (1-503) x US-09-978-697-322 (1-144)

QY 142 CTGACAGTGTATTCGGGGCTGACCTAGACCAAGTTGATTTCTTCTGTGATTTG 201  
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DB 34 LeuLYSThrAspIYrLYSAsnProIleAspGln-----CysAsnThr 47  
QY 202 -----GTTGACCTTTAGACATTTTGTGCCAT--TATATTGCATTAATGATTTA 249  
|||:|||||  
DB 48 LeuAsnProIleValLeuProGluTYrLeuIleHisAlaPhePheCysValMetPheLeu 67  
QY 250 TAAATTAATGATTTAGGTTTGTGCTGAGTACTGAAATAAC-----AGT 297  
|||:|||||  
DB 68 -----CysAlaAlaGluTrpLeuThrLeuGlyLeuAsnMetProIleuLeuAla 83  
QY 298 GAGCATATCTGG--TATATGTCA----- 318  
|||:|||||  
DB 84 TYRHisIleTrpArgTYrMetSerArgProValMetSerGlyProGlyLeuTYrAspPro 103  
QY 319 TTAATTTATGTTAATTAATTAATTTTAAAGTCATGATATAAGGTATGAAACATAT 378  
|||:|||||  
DB 104 ThrThrIleMetAsnAlaAspIleLeuAlaTYrCysGlnLYSGlnGlyTYr----- 120  
QY 379 CATGTAATGACAGATGCAAGTTA--TTTATTTGCTTATTTT 420  
|||:|||||  
DB 121 -----CysLYSLeuAlaPheTYrLeuLeuAlaPhe 130

RESULT 13

US-09-902-941-327  
Sequence 327, Application US/09902941  
Patent No. US20020172952A1  
GENERAL INFORMATION:  
APPLICANT: Henderson, Robert A.  
APPLICANT: Wang, Tongcong  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Johnson, Jeffrey C.  
APPLICANT: Reiter, Marc W.  
APPLICANT: Marnierakis, Margarita  
APPLICANT: Carter, Derrick  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: McNabb, Andria  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C17  
CURRENT APPLICATION NUMBER: US/09/902,941  
CURRENT FILING DATE: 2001-07-10  
NUMBER OF SEQ ID NOS: 2002  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 327  
LENGTH: 144  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-902-941-327  
Alignment Scores:

Pred. No.: 3.68 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
DB: Gaps: 9

US-09-705-500A-1 (1-503) x US-09-902-941-327 (1-144)

QY 142 CTGACAGTGTATTCGGGGCTGACCTAGACCAAGTTGATTTCTTCTGTGATTTG 201  
|||:|||||  
DB 34 LeuLYSThrAspIYrLYSAsnProIleAspGln-----CysAsnThr 47  
QY 202 -----GTTGACCTTTAGACATTTTGTGCCAT--TATATTGCATTAATGATTTA 249  
|||:|||||  
DB 48 LeuAsnProIleValLeuProGluTYrLeuIleHisAlaPhePheCysValMetPheLeu 67  
QY 250 TAAATTAATGATTTAGGTTTGTGCTGAGTACTGAAATAAC-----AGT 297  
|||:|||||  
DB 68 -----CysAlaAlaGluTrpLeuThrLeuGlyLeuAsnMetProIleuLeuAla 83  
QY 298 GAGCATATCTGG--TATATGTCA----- 318  
|||:|||||  
DB 84 TYRHisIleTrpArgTYrMetSerArgProValMetSerGlyProGlyLeuTYrAspPro 103  
QY 319 TTAATTTATGTTAATTAATTAATTTTAAAGTCATGATATAAGGTATGAAACATAT 378  
|||:|||||  
DB 104 ThrThrIleMetAsnAlaAspIleLeuAlaTYrCysGlnLYSGlnGlyTYr----- 120  
QY 379 CATGTAATGACAGATGCAAGTTA--TTTATTTGCTTATTTT 420  
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DB 121 -----CysLYSLeuAlaPheTYrLeuLeuAlaPhe 130

RESULT 14

US-09-978-192A-322  
Sequence 322, Application US/09978192A  
Patent No. US20020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Bacon, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P19  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER:	60/081955
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081817
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081819
PRIOR FILING DATE:	1998-04-15
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PRIOR APPLICATION NUMBER:	60/085322



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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 3.68 length: 144
Score: 75.00 Matches: 13
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 9 Gaps: 9

US-09-705-500a-1 (1-503) x US-09-978-192a-322 (1-144)
QY 142 CTGCAGAGTGATTCGGGGGCTGACCTAGACCACTTGGCATGATCTTCTTGATTTG 201
Db 34 LeuLysThrAspTyrLysAsnProLleAspGln-----CysAsnThr 47
QY 202 -----GTGCATCTTAGACATTTTGTGCCAT---TAAATTGCATTAAGTATTA 249
Db 48 LeuAsnProLeuValLeuProGluTyrLeuIleHisAlaPheheCysValMetPheLeu 67
QY 250 TAAATTAATGATATTAGTTGGCTGAGTACTGGAATAAAC-----AGT 297
Db 68 -----CysAlaIaGluTyrPheThrLeuGlyLeuAsnMetProLeuLeuAla 83
QY 298 GAGCATATCTG---TATATGCA----- 318
Db 84 TyrHisIleTyrArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTTATGTTAAATTACATTTTAAAGTCATGTCATATAAGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnIleAspIleLeuAlaTyrCysGlnLysGluGlyTyr----- 120
QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420
Db 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130

RESULT 15
US-09-999-832a-322
; Sequence 322, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999, 832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-05-05  
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PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637

PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 3.68 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9

US-09-705-500A-1 (1-503) x US-09-999-832A-322 (1-144)

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34 LeuysThraspyrZlysAsnProIleAspGln-----CysAsnThr 47  
::|||  
202 -----GTGCACCTTTAGACATTTTGTGCCAT---TATATTGCATTAATGATTTA 249  
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48 LeuAsnProIleuValIleuProGluTyrLeuIleHisAlaIleAspHehCysValIleProIleu 67  
::|||  
250 TAAATTAATGATATTTAGGTTTGGCTGAGTACTGAATAAAC-----AGT 297  
68 -----CysAlaIleGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83  
|||:|||||  
298 GAGCATATCTGG---TATATGTCA----- 318  
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84 TyrHisIleThrPargTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103  
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319 TTATTATGTTAATTAATTAATTTTAAAGTCATGTCATATCAAGATGATGAACAATAT 378  
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104 ThrThrIleMetAsnAlaIlePleuAlaTyrCysGlnIleuScludIlyTrp----- 120  
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379 CANGTAATGACAGATGCAAGTTA---TTTATTTCCTTATTTT 420  
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Db 121 -----CysIysLeuAlaPheTyrLeuLeuAlaPhe 130

Search completed: November 22, 2004, 18:05:27  
Job time : 277.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2004, 10:37:26 ; Search time 79 Seconds  
(without alignments)  
4525.656 Million cell updates/sec

Title: US-09-705-500a-1  
Perfect score: 503  
Sequence: 1 ccatatcgtctacata.....taataagttcgtttta 503

Scoring table: IDENTITY\_NTC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/6C\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458	91.1	3757	4 US-09-023-655-1502	Sequence 1502, Ap
2	48.6	9.7	7218	1 US-08-232-463-14	Sequence 14, Appl
3	48	9.5	1141	4 US-09-806-708B-22	Sequence 22, Appl
4	48	9.5	640681	4 US-09-790-988-1	Sequence 1, Appl
5	47.8	9.5	1286	4 US-09-601-198-154	Sequence 154, App
6	46.4	9.2	6508	4 US-09-995-917A-2	Sequence 2, Appl
7	45.6	9.1	6669	4 US-10-204-708-6	Sequence 6, Appl
8	45	8.9	6801	4 US-10-204-708-61	Sequence 61, Appl
9	44	8.7	4383	6 5175095-4	Patent No.5175095
10	43.4	8.6	1988	3 US-09-402-002-3	Sequence 3, Appl
11	43.2	8.6	19233	4 US-10-204-708-45	Sequence 45, Appl
12	42.8	8.5	10467	4 US-10-204-708-2	Sequence 2, Appl
13	42.8	8.5	6317	4 US-10-204-708-12	Sequence 12, Appl
14	42.8	8.5	10640	4 US-09-417-485D-5	Sequence 5, Appl
15	41.8	8.3	7304	4 US-10-204-708-43	Sequence 43, Appl
16	41.8	8.3	640681	4 US-09-790-988-1	Sequence 1, Appl
17	41.4	8.2	687	4 US-09-248-796A-8427	Sequence 8427, Ap
18	41.4	8.2	5610	4 US-10-204-708-54	Sequence 54, Appl
19	41.4	8.2	8093	4 US-10-204-708-32	Sequence 32, Appl
20	41.4	8.2	9347	4 US-10-204-708-35	Sequence 35, Appl
21	41.4	8.2	19124	2 US-08-487-826B-13	Sequence 13, Appl
22	41.4	8.2	19513	4 US-10-204-708-39	Sequence 39, Appl
23	41.2	8.2	5152	4 US-10-204-708-73	Sequence 73, Appl
24	41.2	8.2	19233	4 US-10-204-708-46	Sequence 46, Appl
25	41	8.2	8607	4 US-10-204-708-71	Sequence 71, Appl
26	41	8.2	8607	4 US-10-204-708-72	Sequence 72, Appl
27	40.6	8.1	832	4 US-09-621-976-2813	Sequence 2813, Ap

C	28	40.4	8.0	618	3 US-08-953-326-22	Sequence 22, Appl
C	29	40.4	8.0	618	4 US-09-553-662-22	Sequence 22, Appl
C	30	40.4	8.0	618	4 US-10-062-994-22	Sequence 22, Appl
C	31	40.4	8.0	5476	4 US-10-204-708-82	Sequence 82, Appl
	32	40.4	8.0	5562	4 US-10-204-708-63	Sequence 63, Appl
	33	40.4	8.0	6156	4 US-10-204-708-60	Sequence 60, Appl
	34	40.4	8.0	660	1 US-07-991-867B-32	Sequence 32, Appl
	35	40.4	8.0	660	1 US-08-107-755A-32	Sequence 32, Appl
	36	40.4	8.0	660	2 US-08-544-332-32	Sequence 32, Appl
	37	40.4	8.0	660	4 US-09-370-861A-32	Sequence 32, Appl
	38	40.4	8.0	1511	1 US-07-991-867B-8	Sequence 8, Appl
	39	40.4	8.0	1511	1 US-08-107-755A-8	Sequence 8, Appl
	40	40.4	8.0	1511	2 US-08-544-332-8	Sequence 8, Appl
	41	40.4	8.0	1511	4 US-09-370-861A-8	Sequence 8, Appl
	42	40.4	8.0	4810	3 US-08-852-629-11	Sequence 11, Appl
	43	40.4	8.0	4838	3 US-08-852-629-15	Sequence 15, Appl
	44	40.4	8.0	8961	4 US-10-204-708-80	Sequence 80, Appl
	45	40.4	8.0	11049	4 US-10-204-708-22	Sequence 22, Appl

#### ALIGNMENTS

RESULT 1  
US-09-023-655-1502  
Sequence 1502, Application US/09023655  
Patent No. 6607879  
GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSER: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HERMITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1502:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3757 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 9975297  
US-09-023-655-1502  
Query Match 91.1%; Score 458; DB 4; Length 3757;

Best Local Similarity 99.2%; Pred. No. 1.3e-106;  
Matches 502; Conservative 0; Indels 4; Gaps 4;

QY	1	CTATATATGATCTCACTCAATACATATATCTACACATACAGAAAGACAGTCTCCAAAG	60
Db	3244	CTATATATGATCTCAATACATATATCTACACATACAGAAAGACAGTCTCCAAAG	3302
QY	61	TTGCTAGTTTTTGGCTCTCTTTGCCCACTCTCCCTCCAAAT-CCCCCTTAACCT	119
Db	3303	TTGCTAGTTTTTGGCTCTCTTTGCCCACTCTCCCTCCAAATCCCCCTTAACCT	3362
QY	120	CCAAAGCTTCGTCTTGTTGGCTCAGAGTGATTCGGGGAGTACCCTAGACCAAGTTGC	179
Db	3363	CCAAAGCTTCGTCTTGTTGGCTCAGAGTGATTCGGGGAGTACCCTAGACCAAGTTGC	3422
QY	180	ATGATCTCTCTCTTGATTTGGTTGCACCTTAACAATTTTGTGCATTATATTTCAT	239
Db	3423	ATGATCTCTCTCTTGATTTGGTTGCACCTTAACAATTTTGTGCATTATATTTCAT	3482
QY	240	TATGATTTATATTTAATTAATGATTAATTAGTTTGGCTAGTACTAGAAATAAACAGTA	299
Db	3483	TATGATTTATATTTAATTAATGATTAATTAGTTTGGCTAGTACTAGAAATAAACAGTA	3542
QY	300	GCATATCTGGATATATGTCATTTATTTATTTAAATACA-TTTTAAAGCTCCAGTGCAT	358
Db	3543	GCATATCTGGATATATGTCATTTATTTATTTAAATACA-TTTTAAAGCTCCAGTGCAT	3602
QY	359	ATAAAGGTATGAACATATCATGATGATGACATGACATGATTAATTATTTGGCTTA-TT	417
Db	3603	ATAAAGGTATGAACATATCATGATGATGACATGACATGATTAATTATTTGGCTTAATT	3662
QY	418	TTTATATATTAAGATGCCATAGCATATATATGAAAGCTTTGGTAATTCCTCTTAAGATTA	477
Db	3663	TTTATATATTAAGATGCCATAGCATATATATGAAAGCTTTGGTAATTCCTCTTAAGATTA	3722
QY	478	AAATATATTAAGTGTACGTTTTTA 503	
Db	3723	AAATATATTAAGTGTACGTTTTTA 3748	

RESULT 2  
 US-08-232-463-14  
 Sequence 14, Application US/08232463  
 Patent No. 5670367  
 GENERAL INFORMATION:  
 APPLICANT: DORNER, F.  
 APPLICANT: SCHEFFINGER, F.  
 APPLICANT: FALKNER, F. G.  
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
 NUMBER OF SEQUENCES: 52  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 1800 Diagonal Road, Suite 500  
 CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/232,463  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/935,313  
 FILING DATE:  
 APPLICATION NUMBER: EP 91 114 300.6  
 FILING DATE: 26-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.

```

/      REGISTRATION NUMBER : 29,768
/      REFERENCE/DOCKET NUMBER : 30472/114 IMMU
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE : (703)836-9300
/      TELEFAX : (703)683-4109
/      TELEX : 899149
/      INFORMATION FOR SEQ ID NO: 14:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 7218 base pairs
/      TYPE: nucleic acid
/      STRANDEDNESS: single
/      TOPOLOGY: linear
/      IMMEDIATE SOURCE:
/      CLONE: PTGpc-F15
/
US-08-232-463-14

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Query Match	9.7%	Score 48.6	DB 1	Length 7218
Best Local Similarity	8.5%	Pred. No. 0.0061		
Matches	21	Conservative 136	Mismatches 90	Indels 0
Gaps				0
Cy	50	TTCTCACAGTGTGCTAGTTTTCGCTCTCTCTCCCAACCCTACCTCCCAATTC	109	
Db	1229	YY	1288	
Cy	110	CCTTAAACTTCACAGCTGTGCTTGTGCTGCAGAGTATTCGGGGCTGACCTAG	169	
Db	1289	YYY	1348	
Cy	170	ACCAAGTTGCAGATTCCTCTCTGTGATTTGGTGCACCTTAGACATTTTGGCATT	229	
Db	1349	YYY	1408	
Cy	230	ATATTCGATTATGATTTAATTAATGATATTAGGTTTTCGCTGAGTACGAA	289	
Db	1409	YYYYYYYYYYYYYYYYYYYYYGGTACCAATTCCTTCACTCTTAACTACTTGA	1468	
Cy	290	TAAACAG	296	
Db	1469	TAGATAG	1475	

```

RESULT 3
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Parent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAEl promoter
US-09-806-708B-22

```

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Query Match      9.5%  Score 48;  DB 4;  Length 1141;
Best Local Similarity 15.5%  Pred. No. 0.0049;
Matches 75;  Conservative 151;  Mismatches 256;  Indels 3;  Gaps 1;

QY      5  ATATGATCTCAACATATCATATCTATCTACACATACAGAAAGAGAGGCTTCACACATGTGC 64
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      655  ATCAACDIDYASRRYTAACAAATKATTTTTYGBAANNAATYTHNNMGGCANNATDTIRRTWKNNN 714

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QY 65 TAGTTTTTGGCTTCTCTTCCCGCCCTACTCCCTCAATTCCTCCCTTAACCTTCCAA 124
    |||
Db 715 NNAGTWNNNNNNNNAKASAAKYNAAVAAKKGMWMAKMGMAHGAABTTDKRN 774
QY 125 GCTTCGCTCTGTGGTGGCAGAGTATCGGGGGCTGACCTAGACGATTGGCATGAT 184
    |||
Db 775 GATKTTTNNNNNTGVTNTAARGMANNNNNNNNNNNNNGWEDMVTWAAVANYGT 834
QY 185 TCTTCTCTGTGATTTGGTTCGACTTAAACATTTTGGCTCATTAATTTGCAATAT 244
    |||
Db 835 NNNNNNNNNNAAYAMWINKWY---YTTDDHWRBAYTNNNNNNRAAYGAYVADYAYMSDT 891
QY 245 ATTATTAATTAATGAATTTAGTTTGGCTGAGTCTGGAATAAAACAGTGAGACA 304
    |||
Db 892 CDAMWMDATKMNNAATTTKRGITAMRNNNNNNNMTKTYBHAAANNNNNGKMTAHTW 951
QY 305 TCTGTATATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAG 364
    |||
Db 952 WVCATKTTTGGCWNCTTCTCKYKNNCTWYTTTTRTVAATRWKNNATGSMTRCA 1011
QY 365 GTTATGAACATATCATGTAATGACAGATGCAAGTTATTTTATTTGCTTATTTATA 424
    |||
Db 1012 TGKNNNNYWGWTGTPYMAATRMKAMKVMATGSMNTSYARAYKTPAYKGYTVA 1071
QY 425 TTAAGATGCCATAGCATATAATGAAGCTTGTGTAATTCCTTCTAGATAAAATAAT 484
    |||
Db 1072 CAMRWKXATCTMTDNAMWTATCATSMATHKYNWIMCKNNNNNNNNMMWMAAATA 1131
QY 485 AATPA 489
    |||
Db 1132 CDGAR 1136
    |||

RESULT 4
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: MATSUNABE, HIDEKI
; APPLICANT: MATSUNABE, HIDEKI
; APPLICANT: SAKAKI, YOSHIOKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-988-1

Query Match 9.5%; Score 48; DB 4; Length 640681;
Best Local Similarity 50.9%; Pred. No. 0.037;
Matches 114; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
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QY 198 TTTGGTGCCTTAGACATTTTGTGCATTAATTTGCTATGATTAATTAATTAATTA 257
    |||
Db 325119 TTTAATTAATTAATTAATTAATTTTATTCATTAATTAATTTTAAATTAATTAATTA 325178
QY 258 ATGATATTTAGTTTGGCTGAGTCTGGAATTAACAGTGAGACATATCTGTATATGTC 317
    |||
Db 325179 TCTTAATTAATTAATTAATTAATTTAAATGATTAATTAATTAATTAATTAATTTT 325238
QY 318 ATTATTTATTTGTTAATTAATTAATTTTAACTCCATGTCATTAATTAAGTTATGAACATA 377
    |||
Db 325239 ACATTTTATTAATTAATTAATTAATTAATTTTAAATTTTAAATTAATTAATTAATTA 325298
QY 378 TCATGTAATGACAGATGCAAGTATTTTATTTGCTTATTTTAA 421
    |||
```

```
Db 325299 TTAATTAATTAATTAATTAATTAATTTTCTTTTATTTTAA 325342
    |||

RESULT 5
US-09-601-198-154/c
; Sequence 154, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Caselli, Gail H.
; APPLICANT: Chen, Eileen Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; FILE REFERENCE: UREAPLITCDM
; CURRENT APPLICATION NUMBER: US/09/601,198
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
; US-09-601-198-154

Query Match 9.5%; Score 47.8; DB 4; Length 1296;
Best Local Similarity 51.3%; Pred. No. 0.0056;
Matches 139; Conservative 0; Mismatches 127; Indels 5; Gaps 1;
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QY 162 TGACCTAGACAGTTGGCATGATCTTCTCTGATTTGGTGCATTTAGCATTTT 221
    |||
Db 272 TTAATTAATTAATTAATTAATTTTCTGATTTTTCATCAATTAACATTAACATTAATTAAGTT 213
QY 222 GTGCATTAATTTGCTATTAATTAATTTAATTAATTAATTAATTAATTTTGGCTGAG 281
    |||
Db 212 TTTTATCATTTTAAAGTGTGATCAACATTAACATTAACATTAACATTTTGGATTTA 153
QY 282 TACTGATTAATTAACAGTGCATATCTGTATATGCTATTTATTTGTTAATTAATTA 341
    |||
Db 152 TCCATTAATTAATTAATTAATTTGATTTATTTGTTAATTTGTTTAAATTTG---- 98
QY 342 TTAACCTCAGTGCATTAATTAAGTTATGAACAATCATCATGTAATGACAGATGCAAGTT 401
    |||
Db 97 ATGCTCATGAGAGGTGATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 38
    |||
QY 402 ATTTATTTGCTTATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 432
    |||
Db 37 ATTTAGTATGATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7
    |||

RESULT 6
US-09-995-917A-2/c
; Sequence 2, Application US/09995917A
; Patent No. 6768043
; GENERAL INFORMATION:
; APPLICANT: WANG
; TITLE OF INVENTION: DASS, A P450 PROTEIN INVOLVED IN THE
; FILE REFERENCE: SALKINS-045A
; CURRENT APPLICATION NUMBER: US/09/995,917A
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 6508
; TYPE: DNA
; ORGANISM: DASS
; US-09-995-917A-2
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	Query Match	Similarity	Score	DB	Length
Best Local Match	9.2%	50.3%	46.4	4	6508
Matches	145	Conservative	0	Mismatches	136
				Indels	7
				Gaps	1

OY	316	TCATTATTATTATGTTAAATTCATTTTTAAAGCTCCAGTCGACATGAAGTTAAGTTAAGACA	375
Db	6147	ATTTTTTATTATTGTTTGGTTTGTATATATAGTATTGTGTAATATATTTTTTATTATTTAA	6206
OY	376	TATCATGTGTAATGCACAGATGCAACTTATTATTTCCTTATTTTTATATTAAGAATGCC	435
Db	6207	GTAATATGTATATTTTAAGATAGTAAGAAATTTGTTTTTTGTTATTTGTGTGATTTAGTAATATA	6266
OY	436	ATAGCATAAATATGAAAGCTTTGGTGA-ATTCCTTCTAAGATTAATAATATATTAAGTGT	494
Db	6267	AGATTAATATAAGTACGGTTTTTTTAAAGATTATTGTATGTTTAAAGAAATATTAATAT	6326
OY	495	TACGTTTT 502	
Db	6327	TAATTTT 6334	
RESULT 8			
US-10-204-708-61			
; Sequence 61, Application US/10204708			
; Patent No. 6677731			
; GENERAL INFORMATION:			
; APPLICANT: OLEK, Alexander			
; APPLICANT: PIEPENROCK, Christian			
; APPLICANT: BERLIN, Kurt			
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication			
; TITLE OF INVENTION: by Assessing DNA Methylation			
; FILE REFERENCE: 5013.1012			
; CURRENT APPLICATION NUMBER: US/10/204,708			
; PRIOR FILING DATE: 2003-05-06			
; PRIOR APPLICATION NUMBER: PCT/EP01/03971			
; PRIOR FILING DATE: 2001-04-06			
; PRIOR APPLICATION NUMBER: DE 10019058.8			
; PRIOR FILING DATE: 2000-04-06			
; PRIOR APPLICATION NUMBER: DE 10019173.8			
; PRIOR FILING DATE: 2000-04-07			
; PRIOR APPLICATION NUMBER: DE 10032529.7			
; PRIOR FILING DATE: 2000-06-30			
; PRIOR APPLICATION NUMBER: DE 10043826.1			
; PRIOR FILING DATE: 2000-09-01			
; NUMBER OF SEQ ID NOS: 98			
; SEQ ID NO 61			
; LENGTH: 6801			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)			
US-10-204-708-61			
Query Match 8.9%; Score 45; DB 4; Length 6801;			
Best Local Similarity 52.9%; Pred. No. 0.049;			
Matches 119; Conservative 0; Mismatches 105; Indels 1; Gaps 1;			
OY	209	TTTAGACATTTTGTGCGCATTATTTTGCATTATGTATATATTTAAATGAATTTAG	268
Db	6390	TTTATATATTGAGGTTAAATTTATATATAGATATTTTTTTATTAGTTTTTTTG	6449
OY	269	GTTTTGGCGAGTACTGGAATPAAACGTGACATCTGGTATATCTCATTTATTG	328
Db	6450	ATTTTTTTTGTGTTTGTATGTTTTTAAAGGTAAGGTTATATATTTTTTTTAGGTG	6509
OY	329	TTAATATACATTTTAAAG-CTCCATGTGCATATPAAAGGTTATGAACATATCATGTAAAT	387
Db	6510	TTATTTTTTAAATTTTAAATGTAGATTTTTGTGATATATTTATATATATATATATTATT	6569
OY	388	GACAGATGCAAGTTATTTTATTGCTTATTTTTTAAATTAAGAT	432
Db	6570	TGTGAATAGATGTTGTTTATTTTTTTTTTTTATTTTATGTT	6614
RESULT 9			
US-175095-4/c			

Patent No. 5175095  
APPLICANT: Martineau, Belinda M./Houck, Catherine M.  
TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS  
NUMBER OF SEQUENCES: 9  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/554,195  
FILING DATE: 17-JUL-1990  
SEQ ID NO: 4  
LENGTH: 4383  
5175095-4

Query Match 8.7%; Score 44; DB 6; Length 4383;  
Best Local Similarity 48.8%; Pred. No. 0.076;  
Matches 119; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 242 TGTATTATATATTAATGATATTTAGTTTGGCTGAGTACTGGAATMAACAGTACG 301  
D 1525 TGTATATACCTGATTTTATTTATTTTGGTGGTACATCATTTAGTATTTGG 1466  
QY 302 ATATCTGGTATATGTCATTTATTTGTTAATTACATTTTAAGCTCCATGTGATATA 361  
D 1465 CAATAGACATATTTTATTTTATTTAGCAAAAATCATCTTTAATTGAATGGGTGAGTA 1406  
QY 362 AAGGTATGAACATATCATGTATGACAGATGCAAGTATTTTATTTGCTTATTTTA 421  
D 1405 CATTAGATATTTAGATTTCTAGCTATGATTTGTAATAATAGTTTGTGTGGAATATTTTA 1346  
QY 422 TAAATTAAGATGCCATATGATTAATATGAAAGCCTTGGTGAATCCTTGAATATAAAT 481  
D 1345 CCCATTAATGTGAGACACCTCTACAGATATTAATTAATTTCTAATATGATGT 1286  
QY 482 AATA 485  
D 1285 CAAA 1282

RESULT 10  
US-09-402-002-3/C  
Sequence 3, Application US/09402002  
Patent No. 6225453  
GENERAL INFORMATION:  
APPLICANT: Ueyama, Hiroshi  
APPLICANT: Abe, Kanako  
APPLICANT: Keshi, Hiroyuki  
APPLICANT: Matsubisa, Aki  
TITLE OF INVENTION: PROBES FOR THE DIAGNOSIS OF INFECTIONS  
TITLE OF INVENTION: CAUSED BY KLEBSIELLA PNEUMONIAE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive/6300 Sears Tower  
City: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
Zip: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,002  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 1997-71082  
FILING DATE: 25-MAR-1997  
PRIOR APPLICATION DATA: PCT/JP98/01286  
FILING DATE: 23-MAR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Cawley, Jr., Thomas A.  
REGISTRATION NUMBER: 40,944

REFERENCE/DOCKET NUMBER: 19036/36276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1988 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Klebsiella pneumoniae  
STRAIN: Clinical Isolate KP-98-22  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1930  
OTHER INFORMATION: /note="N= adenine or cytosine or  
OTHER INFORMATION: guanine or thymine"

Query Match 8.6%; Score 43.4; DB 3; Length 1988;  
Best Local Similarity 50.7%; Pred. No. 0.083;  
Matches 104; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 228 TTATTTTGCATATGATTTTATTAATTAATTAATTAATTTAGTTTGGCTGACTG 287  
D 206 TCATTTTATCTCTCTGTTTCTGTCATTTTAAATTAATTAATTAATTAATTAATTTGT 147  
QY 288 AATAACGATGACATATCTGATATGTCATTTATTTGTTAATTATACATTTTAAAC 347  
D 146 CAATATATTTATACACATCTTGACTATATTAATTTGTTTATTTATTAATGTAAC 87  
QY 348 TCCATGTGCATATAAGGTATGAAACATATCATGTATGACAGATGCAAGTATTTTA 407  
D 86 CAATATAAATAATAAGATAGCAACCAATATAACATCAAAATGAGAAAGTATGAG 27  
QY 408 TTGCTTATTTTATTAATTAAGAT 432  
D 26 AAGAAAAATCTTTTATTTCTAAGCT 2

RESULT 11  
US-10-204-708-45  
Sequence 45, Application US/10204708  
Patent No. 6677731  
GENERAL INFORMATION:  
APPLICANT: Oler, Alexander  
APPLICANT: PIERENROCK, Christian  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
TITLE OF INVENTION: by Assessing DNA Methylation  
FILE REFERENCE: 5013.1012  
CURRENT APPLICATION NUMBER: US/10/204,708  
CURRENT FILING DATE: 2003-05-06  
PRIOR APPLICATION NUMBER: PCT/EP01/03971  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: DE 10019058.8  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 98  
SEQ ID NO 45  
LENGTH: 19233  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
FEATURE:

NAME/KEY: unsure  
LOCATION: (76, 178..179, 273, 586, 648, 651, 920, 1014, 1173, 1197, 1228)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (2168, 2254, 2257, 2280, 2291, 2723, 3018, 3080, 4205, 4209)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (4216, 4225, 4239, 4246, 4254, 4265, 4270, 4274, 4288, 4294..4295)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (4298, 4363, 4610, 4627, 4675, 4693, 4698, 4738, 4777, 4781)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (4787, 4825, 4829, 4838, 4855, 5462, 5494, 5496, 5500, 5674)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (5690, 5697, 5705, 5715, 5890, 5910, 5913, 6027, 6080, 6109)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (6244, 6288, 6776, 6873, 6891, 6980, 7028, 7656, 7876, 8030)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (8059, 8075, 8632, 8636, 9700, 9717, 9815, 9818, 9867, 9879)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (10005, 10075, 10150, 10159, 10165, 10356, 11123, 11166, 11360)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (11703, 11933, 12050, 12340, 12981, 13564, 13764..13765, 13787)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (13846, 14168, 16566, 17006, 17217, 17650, 17653, 17656, 17898)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (18130, 18143, 18151, 18188, 18498, 18549, 18936, 18946, 19165)  
OTHER INFORMATION: n is a or g or c or t  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (19200)  
OTHER INFORMATION: n is a or g or c or t  
US-10-204-708-45

Query Match 8.6%; Score 43.2; DB 4; Length 19233;  
Best Local Similarity 47.5%; Pred. No. 0.19;  
Matches 150; Conservative 0; Mismatches 164; Indels 2; Gaps 1;

QY 175 TTTCGATGATTCCTCCTGATTTGGTGCATTTAGACATTTTGTGCGCATTTAT 234  
DB 1588 TTTCGATTTTATGTTTTTTTGTGTTAGTTTTTTTATTTATTTAGTTTATTTAT 1647  
QY 235 TGCAATTAGTATTATTAATTAATGATATTAGTTTTGCTGAGTACTGGAATTAAC 294  
DB 1648 GTGATATTATTATTATTTGATTTGGGNTTGGGTTAGATTGTGATTTTAAAGA 1707  
QY 295 AGTAGATATCTGCTATGCTATTTATTTATTTAAATTAATTAATTTAAGCTCAGT 354  
DB 1708 TTAAGTCGTTTTTTTAAAGTTATTTGAATTTGATTTTAAATATTATGTT 1767

QY 355 GCATTAAGGTTATGAAACATA--TCATGTTATGACAGATGCAAGTTATTTATTTGC 412  
DB 1768 TAGATATAGCTTAGGATGATGCTTACCTTTGATTTTGTATTTTGGATGTTGGT 1827  
QY 413 TTATTTTATTAATTAAGATGCGATAGCATATATGAAAGCTTTGGTGAATTCCTTAA 472  
DB 1828 GGATTTATTTAGATTTGAGATTTTATGTTTATTTGTTAAATCGGTGAATTTATTT 1887  
QY 473 GATTAATTAATTAATA 488  
DB 1888 TATTAAATATTAATAA 1903

RESULT 12  
US-10-204-708-2

; Sequence 2, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIERENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; TITLE OF INVENTION: by Assessing DNA Methylation  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; PRIOR FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 2  
; LENGTH: 10467  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-2

Query Match 8.5%; Score 43; DB 4; Length 10467;  
Best Local Similarity 49.3%; Pred. No. 0.18;  
Matches 112; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 216 ATTTTGGCATTATATTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTTAG 275  
DB 478 ATTTTTTTAAAGTTAGTTATTTAGTGAATTTTGTATTGTTTATTTGTTTAAAGATTATC 537  
QY 276 GCTAGTACTGGAATTAACAGTGAATCTGATATGCTATTTATTTTGTAAAT 335  
DB 538 GTTTAGATGATTAATTAAGAAAGAAATGATTTGATTAATTTGATTTT 597  
QY 336 ACATTTTAAAGCTCATGTCATTAAGGTTATGAACATATCATGTTATGACAGATG 395  
DB 598 AAGTTGTAAGCTGTAACGAATTAATTTTATTTAGTGGAAAGTTAGCGAATTT 657  
QY 396 CAAGTATTTATTTGCTTATTTTATTAATTAAGATGCCATAGCAT 442  
DB 658 AGAGTATTTTGTGTTTTTATTTATTTAGGAGGATTTGAAT 704

RESULT 13  
US-10-204-708-12  
; Sequence 12, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIERENBROCK, Christian



```

; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 12
; LENGTH: 6317
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-12

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Query Matchsimilarity	8.5%	Score 42.8	DB 4	Length 6317
Best Local Similarity	49.0%	Pred. No. 0.17		
Matches 142, Conservative	0	Mismatches 147	Indels 1	Gaps 1

QY	205	GCACCTTAGACATTTTGGCCATTAATATTCGATTAGTAATTAATTTAAATGAT	265
Db	473	GAAGTTAGAAATGTAATAAATAGAGTTGCTTTTATAGTAATTAATAGTTGT	533
QY	265	TTAGTTTTTGGCTGAGTACGAAATAAACAGTGACATCTGGTATATGCAATTT	324
Db	533	ATTTTTTAATGATAGTGTTTTTTGAAGAGTTTGTAATTAATATAGTTTTTAAT	592
QY	325	ATTGTAATTAATATTTTAAGTCCAGTGCATATAAAGGTATAGAAATATCATGG	383
Db	593	AGTTTTTAAGATTTGTATAAAGGTTATATTTTGAAGAAAGATGAAACGTTAAATTA	652
QY	384	TAAATGACAGTGCAGTTATTTTATTTGCTATTTTATTAATTAAGAATCCATAGATA	443
Db	653	TTTCGAGACGATTTTATTATATAATTTGTTTTTTTATATTTAAGTGTGACGTAAAGAT	712
QY	444	ATTGGAAGCCTTTTGCAATTCCTCTTAAGATATAAAATATATATNAAGTG	493
Db	713	ATATTTTTTAAGGCGTTTAAATATTTTATTAATGAGGAAATAAGTATATTGG	762

```

RESULT 14
US-09-417-485D-5/c
Sequence 5, Application US/09417485D
Patent No. 6541202
GENERAL INFORMATION:
APPLICANT: Long, David M.
APPLICANT: Metz, Anneke M.
APPLICANT: Love, Ruscabelle A.
TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
FILE REFERENCE: 47714-5009-US
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 10640
TYPE: DNA
ORGANISM: Plasmodium falciparum
FEATURE:
NAME/KEY: CDS
LOCATION: (834)..(7385)
OTHER INFORMATION: TERT gene
FEATURE:

```

```

? NAME/KEY: unsure
? LOCATION: (1821).. (1837)
? OTHER INFORMATION: m at position 1821 = a or c; w at position 1837 =
? OTHER INFORMATION: a or t. Xaa (amino acid) at position 330 = Leu or
? OTHER INFORMATION: Ile; Xaa at position 335 = Asp or Gly.
US-09-417-485D-5

```

Query Match	8.5%	Score	42.8	DB	4	Length	10640
Best Local Similarity	48.4%	Pred. No.	0	2			
Matches	119	Conservative	0	Mismatches	127	Indels	0
						Gaps	0

QY	184	TTCTCTCCCTGGATTTGGTGGCACTTTAGACATTTTGGCCATTTATTTGGATTATG	243
Db	2841	TTTTTTTATTAATATTTTATGATACATTTATTTGTTATGATTTCCCTATTTATTTG	2782
QY	244	TATTTATATATTTAAATGATATTTAGGTTTTGGCTGAGTACTGGAATPAACAGTGAGCAT	303
Db	2781	TATGTAATAAATTTGGTTTTTCATAGTTGTATCAAAATATATTTCTTAATAAATATCTATTTT	2722
QY	304	ATCGGAAATATGTCATATTTATTTGTAAATTTACATTTTAAAGCTGCATGCGCATPAAA	363
Db	2721	TTATATTAATTTTACTATTTTATTTTGGAAATATATTTTACTTAATATTTTTCATTA	2662
QY	364	GGTTATGAAACATATCATGCTAAATGACAGATGCAAGTTATTTATTTTGTATTTTATA	423
Db	2661	CTTGATTTTAAAGAAAACTTCTTTAATTAATTAATAACAAAAATTTTTTTACATTTTATA	2602
QY	424	ATTAAA	429
Db	2601	AAAAATA	2596

RESULT 15  
US-10-204-708-43

```

Patent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 43
LENGTH: 7304
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OS-10-204-708-43

```

Query Match	8.3%	Score 41.8	DB 4	Length 7304
Best Local Similarity	47.9%	Pred. No. 0.32		
Matches 152	Conservative 0	Mismatches 162	Indels 3	Gaps 1
QY	167	TTCTCTGTGATTTGGTTCGACCTTTAGACATTTTGTGCATATATTTTCGATATAGT	246	
Db	515	TTCAGTTTTTTTTTGTGCGCTTTAGGTTCGAGTATAGGTTATATATATATCGCTTATATTGTA	574	
QY	247	TTATATATTAATGATATTAGGTTTTTGGCTGAGTACTGGAATAAACAAGTAGGACATATC	306	

